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Query Match 100.0%; Score 609; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-081-056-6
; Sequence 6, Application US/10081056
; Publication No. US2004043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C1
; CURRENT APPLICATION NUMBER: US/10/081.056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
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; PRIOR APPLICATION NUMBER: US 09/643,657
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;; PRIOR FILING DATE: 2001-06-28
;; NUMBER OF SEQ ID NOS: 383
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;; LENGTH: 117
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US-10-081-056-6

Query Match 100.0%; Score 609; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 QOAEASVPTADTRSQPRDVPVPRGRGPHEPRKKQNVGLVLDTLAVIRTLVDK 117

RESULT 3
US-10-066-500-9
; Sequence 9, Application US/10066500
; Publication No. US20020177165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Aehkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Bostein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
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; PRIOR APPLICATION NUMBER: PCT/US99/21547

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Query Match 100.0%; Score 609; DB 13; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-002-796-9
; Sequence 9, Application US/10002796
; Publication No. US20030032057A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
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; APPLICANT: Nicholas F. Paoni
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; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watarabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C1
; CURRENT APPLICATION NUMBER: US/10/002.796
; CURRENT FILING DATE: 2001-11-15
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 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301

Query Match 100.0%; Score 609; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGATTWGNSCICRDSGTTDSVDTQQ 60
 Dd 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGATTWGNSCICRDSGTTDSVDTQQ 60
 Qy 61 QQAENSAVPTADTRSQRPDPVPRRGRGPHPRKKQNVGLVLTFLAVITLVDK 117
 Dd 61 QQAENSAVPTADTRSQRPDPVPRRGRGPHPRKKQNVGLVLTFLAVITLVDK 117

RESULT 5

US-10-066-273-9

Sequence 9, Application US/10066273

Publication No. US20030032062A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi

APPLICANT: Kevin P. Baker

APPLICANT: David A. Botstein

APPLICANT: Luc Desnoyers

APPLICANT: Dan L. Eaton

APPLICANT: Napoleon Ferrara

APPLICANT: Sherman Fong

APPLICANT: Wei-Qiang Gao

APPLICANT: Hanspeter Gerber

APPLICANT: Mary E. Gerritsen

APPLICANT: Audrey Goddard

APPLICANT: Paul J. Godowski

APPLICANT: Austin L. Gurney

APPLICANT: Ivar J. Kljavin

APPLICANT: Jennie P. Mather

APPLICANT: Mary A. Napier

APPLICANT: James Pan

APPLICANT: Nicholas F. Paoni

APPLICANT: Margaret Ann Roy

APPLICANT: Timothy A. Stewart

APPLICANT: Daniel Tomas

APPLICANT: Colin K. Watanabe

APPLICANT: P. Mickey Williams

APPLICANT: William I. Wood

APPLICANT: Zemin Zang

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ACIDS ENCODING THE SAME

FILE REFERENCE: P3130R1C2

CURRENT APPLICATION NUMBER: US/10/066,273

CURRENT FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 10/002,796

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062285

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062816

PRIOR FILING DATE: 1997-10-24

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PRIOR FILING DATE: 1997-10-31

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PRIOR APPLICATION NUMBER: 60/063733

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/06364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/066840

PRIOR FILING DATE: 1997-11-25

PRIOR APPLICATION NUMBER: 60/069694

PRIOR FILING DATE: 1997-12-15

PRIOR APPLICATION NUMBER: 60/074086

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: 60/074092

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PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/081049

PRIOR FILING DATE: 1998-04-08

PRIOR APPLICATION NUMBER: 60/095998

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PRIOR APPLICATION NUMBER: 60/097000
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; PRIOR FILING DATE: 1999-10-18
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; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

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Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGGLLLTLEEHIAHPLGTGGATTMGNSICRDDSGTDDSDVDYQQ 60
Db 1 MIVFGWAVFLASRLGGLLLTLEEHIAHPLGTGGATTMGNSICRDDSGTDDSDVDYQQ 60

QY 61 QQAENSAVPTADTRSPQRPDPVPRRGPHPRKKQNVGGLVLDTLAVITLVDK 117
Db 61 QQAENSAVPTADTRSPQRPDPVPRRGPHPRKKQNVGGLVLDTLAVITLVDK 117

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RESULT 6

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US-10-066-494-9
; Sequence 9, Application US/10066494
; Publication No. US20030032063A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C9
; CURRENT APPLICATION NUMBER: US/10/066,494
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 1998-09-09
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 ; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MIVFGWAVFLASRSLGQGLLLTLEBHHAFILGTGGAATTMGNSCICRDDSGTDDSDVDTQQ 60
 DB 1 MIVFGWAVFLASRSLGQGLLLTLEBHHAFILGTGGAATTMGNSCICRDDSGTDDSDVDTQQ 60
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 DB 61 QQAENSAPVTADTRSQPRDPVPRRGRGPHEPRRKKQNVGLVLDLTLAVIRTLVXK 117

 RESULT 7
 US-10-066-269-9
 ; Sequence 9, Application US/10066269
 ; Publication NO. US20030040014A1

GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerlitsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: F. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C4
CURRENT APPLICATION NUMBER: US/10/066,269
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
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PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/423844

APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: F. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C8
CURRENT APPLICATION NUMBER: US/10/066,211
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1999-04-15
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PRIOR APPLICATION NUMBER: 09/423844
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 ; PRIOR APPLICATION NUMBER: 09/886342
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 ; PRIOR APPLICATION NUMBER: PCT/US98/19093
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 ; PRIOR APPLICATION NUMBER: PCT/US99/20111
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 ; PRIOR FILING DATE: 1999-09-08
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 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e-58;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MIVFGWAVFLASRLGQLLTLLEEHIAHFLGTGGAATTWNSICRDDSVDVTDQ 60
 Db 1 MIVFGWAVFLASRLGQLLTLLEEHIAHFLGTGGAATTWNSICRDDSVDVTDQ 60
 Qy 61 QOENSAPVPTADTSQRPDPVRRGRGPHPEPRKKQNDGLVLDPLAVIRTLVDK 117
 Db 61 QOENSAPVPTADTSQRPDPVRRGRGPHPEPRKKQNDGLVLDPLAVIRTLVDK 117

RESULT 10
 US-10-066-193-9
 ; Sequence 9, Application US/10066193
 ; Publication No. US2003004902A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Avi J. Ashkenazi
 ; APPLICANT: Kevin P. Baker
 ; APPLICANT: David A. Botstein
 ; APPLICANT: Luc Desnoyers
 ; APPLICANT: Dan L. Eaton
 ; APPLICANT: Napoleone Ferrara
 ; APPLICANT: Sherman Fong
 ; APPLICANT: Wei-Qiang Gao
 ; APPLICANT: Hanspeter Gerber
 ; APPLICANT: Mary E. Gerritsen
 ; APPLICANT: Audrey Goddard
 ; APPLICANT: Paul J. Godowski
 ; APPLICANT: Austin L. Gurney
 ; APPLICANT: Ivar J. Kjavlin
 ; APPLICANT: Jennie P. Mather
 ; APPLICANT: Mary A. Napier
 ; APPLICANT: James Pan
 ; APPLICANT: Nicholas F. Paoni
 ; APPLICANT: Margaret Ann Roy
 ; APPLICANT: Timothy A. Stewart
 ; APPLICANT: Daniel Tumas

; APPLICANT: Colin K. Watanabe
 ; APPLICANT: P. Mickey Williams
 ; APPLICANT: William I. Wood
 ; APPLICANT: Zemin Zang
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3130R1C3
 ; CURRENT APPLICATION NUMBER: US/10/066,193
 ; CURRENT FILING DATE: 2002-02-01
 ; PRIOR APPLICATION NUMBER: 10/002,796
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
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;; PRIOR APPLICATION NUMBER: 09/808689
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;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 09/870574
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: 09/872035

;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/886342
;; PRIOR FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: PCT/US98/14552
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;; PRIOR APPLICATION NUMBER: PCT/US98/25190
;; PRIOR FILING DATE: 1998-11-25
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDSGTDSDVDTOQ 60
Db 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDSGTDSDVDTOQ 60
Qy 61 QQAENSAVPTADTRSPQRPVPRPRGRGPHEPRKKQNVGLVLTFLAVIRTLVDK 117
Db 61 QQAENSAVPTADTRSPQRPVPRPRGRGPHEPRKKQNVGLVLTFLAVIRTLVDK 117
RESULT 11
US-10-006-818A-6
; Sequence 6, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deansoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Wei-Qiang
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PR1

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-16
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22-26, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-006-818A-6

Query Match      100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60
Db      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60

Qy      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117
Db      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117

RESULT 12
US-10-015-393A-6
; Sequence 6, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-16
; OTHER INFORMATION: Signal Peptide
; NAME/KEY: misc feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22-26, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-015-393A-6

Query Match      100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60
Db      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60

Qy      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117
Db      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117

RESULT 13
US-10-015-869A-6
; Sequence 6, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-16
; OTHER INFORMATION: Signal Peptide
; NAME/KEY: misc feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22-26, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-015-869A-6

Query Match      100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60
Db      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60

Qy      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117
Db      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117

RESULT 14
US-10-012-121A-6
; Sequence 6, Application US/10012121A
; Publication No. US20030073810A1
; Publication No. US20030073810A1

Query Match      100.0%; Score 609; DB 14; Length 117;
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Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60
Db      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60

Qy      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117
Db      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117

RESULT 13
US-10-015-869A-6
; Sequence 6, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-16
; OTHER INFORMATION: Signal Peptide
; NAME/KEY: misc feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22-26, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-015-869A-6

Query Match      100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60
Db      1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDSGTDDSDVDTQQ 60

Qy      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117
Db      61 QOAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVLDGLVLTAVIRTLVDK 117

RESULT 14
US-10-012-121A-6
; Sequence 6, Application US/10012121A
; Publication No. US20030073810A1
; Publication No. US20030073810A1

Query Match      100.0%; Score 609; DB 14; Length 117;
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; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
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; PRIOR APPLICATION NUMBER: 60/101475
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; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
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; PRIOR APPLICATION NUMBER: 60/102570
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; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07

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; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105981
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105982
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

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Query Match 100.0%; Score 609; DB 14; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-58;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MIVFGWAVFLASRSIGQGLLTLESHIAHFLGTGGAATTMGNSCICRDDSGTDDSDVDIQQ 60
Db 1 MIVFGWAVFLASRSIGQGLLTLESHIAHFLGTGGAATTMGNSCICRDDSGTDDSDVDIQQ 60
QY 61 QQAENSAPVTADTRSQRPDPVPPRGRGPPEPRKKQNVLDGLVLDTLAVIRTLVDK 117
Db 61 QQAENSAPVTADTRSQRPDPVPPRGRGPPEPRKKQNVLDGLVLDTLAVIRTLVDK 117

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Search completed: April 2, 2004, 10:32:34

Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 2, 2004, 10:28:10 ; Search time 22 Seconds
(without alignments)
274.556 Million cell updates/sec

Title: US-10-002-796-9
Perfect score: 609
Sequence: 1 MIVFGWAVFLASRLGQGLL.....QNVGILDTLAVITLVDK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/prodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	13.1	460	4	US-09-252-991A-20180
2	79	13.0	287	4	US-09-252-991A-30267
3	78	12.8	1527	4	US-09-418-710-27
4	78	12.8	1531	4	US-09-418-710-29
5	75	12.3	433	2	US-08-466-120-2
6	75	12.3	433	5	PCT-US94-07266-2
7	75	12.3	1525	4	US-09-418-710-69
8	74.5	12.2	462	2	US-08-865-597A-2
9	73.5	12.1	2509	2	US-08-149-097D-35
10	73	12.0	623	3	US-09-029-348-3
11	73	12.0	626	3	US-09-029-348-2
12	72.5	11.9	333	4	US-09-252-991A-28443
13	71.5	11.7	562	4	US-09-252-991A-20178
14	71.5	11.7	566	4	US-09-252-991A-18531
15	71	11.7	863	4	US-09-252-991A-26099
16	70	11.5	396	4	US-09-252-991A-32927
17	69	11.3	191	2	US-08-390-665A-198
18	69	11.3	191	2	US-08-390-665A-199
19	69	11.3	191	2	US-08-390-665A-200
20	69	11.3	191	2	US-08-390-665A-201
21	69	11.3	191	2	US-08-390-665A-202
22	69	11.3	191	2	US-08-390-665A-203
23	69	11.3	191	5	PCT-US95-10398-198
24	69	11.3	191	5	PCT-US95-10398-199
25	69	11.3	191	5	PCT-US95-10398-200
26	69	11.3	191	5	PCT-US95-10398-201
27	69	11.3	191	5	PCT-US95-10398-202

Sequence 203, App
Sequence 226, App
Sequence 226, App
Sequence 19537, A
Sequence 2, Appli
Sequence 508, App
Sequence 4, Appli
Sequence 21599, A
Sequence 31693, A
Sequence 78, Appl
Sequence 18753, A
Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli

28 69 11.3 191 5 PCT-US95-10398-203
29 69 11.3 319 4 US-08-635-886C-226
30 69 11.3 319 4 US-08-974-690C-226
31 69 11.3 350 4 US-09-252-991A-19537
32 69 11.3 498 4 US-09-354-151-2
33 69 11.3 778 4 US-09-198-452A-508
34 69.5 11.2 788 2 US-08-918-914-4
35 68 11.2 149 4 US-09-252-991A-21599
36 68 11.2 379 4 US-09-252-991A-31693
37 68 11.2 882 3 US-09-413-814-78
38 67.5 11.1 518 4 US-09-252-991A-18753
39 67.5 11.1 727 2 US-08-475-844-9
40 67.5 11.1 727 5 PCT-US95-08429-9
41 67.5 11.1 1298 2 US-08-630-473-2
42 67.5 11.1 1298 3 US-09-259-821A-2
43 67.5 11.1 1298 3 US-08-843-659-2
44 67 11.0 393 4 US-09-432-470-2
45 67 11.0 393 4 US-09-432-470-4

ALIGNMENTS

RESULT 1
US-09-252-991A-20180
; Sequence 20180, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20180
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20180

Query Match 13.1%; Score 80; DB 4; Length 460;
Best Local Similarity 28.6%; Pred. No. 0.42;
Matches 20; Conservative 11; Mismatches 23; Indels 16; Gaps 2;
QY 32 GTGAATTMGNSICRDSGTDDSDTQQQAENSAVPTADTRSQPRDPVPPRRGRGPH 91
DB 373 GCGQAQVQAG-----EQADPEQRRVPGEAQIA-----NRGDPVPPGERRGDH 416
QY 92 EPRRKKQNV 101
DB 417 EQQRQGRHVD 426

RESULT 2
US-09-252-991A-30267
; Sequence 30267, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30267
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30267

Query Match      13.0%; Score 79; DB 4; Length 287;
Best Local Similarity 37.5%; Pred. No. 0.3;
Matches 21; Conservative 7; Mismatches 24; Indels 4; Gaps 1;

QY 51 GTDSDVDTQCOQAENS AVPTADTRSQPRDPVPP-----RRGRGPHPRKXQNVG 102
Db 15 GRDPGRRTQRRRDHPAGVAVARPGARRRRPGGLAGRGGRGAGKRRRRRQVPG 70

RESULT 3
US-09-418-710-27
; Sequence 27, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-27

Query Match      12.8%; Score 78; DB 4; Length 1527;
Best Local Similarity 27.5%; Pred. No. 3.5;
Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;

QY 48 DSGTDSVDTQCOQAENS AVPTADTRSQPRDPVR-----PP-----RRGRGPHPRR 95
Db 1255 EDESDEEEEEEEDYEVAGLRPRKTRTKIRGKHSVIPPAARSGRRPGKPKHSTR 1314

QY 96 KK-----QNVDTGLVLD 107
Db 1315 SQKAPVDDAEVDVLTQ 1334

RESULT 4
US-09-418-710-29
; Sequence 29, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1531

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-29

Query Match      12.8%; Score 78; DB 4; Length 1531;
Best Local Similarity 27.5%; Pred. No. 3.5;
Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;

QY 48 DSGTDSVDTQCOQAENS AVPTADTRSQPRDPVR-----PP-----RRGRGPHPRR 95
Db 1259 EDESDEEEEEEEDYEVAGLRPRKTRTKIRGKHSVIPPAARSGRRPGKPKHSTR 1318

QY 96 KK-----QNVDTGLVLD 107
Db 1319 SQKAPVDDAEVDVLTQ 1338

RESULT 5
US-08-466-120-2
; Sequence 2, Application US/08466120
; Patent No. 5869284
; GENERAL INFORMATION:
; APPLICANT: CAO, ET AL.
; TITLE OF INVENTION: Retinoic Acid Receptor Epsilon
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/466,120
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07366
; FILING DATE: 24 JUN 94
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-466-120-2

Query Match      12.3%; Score 75; DB 2; Length 433;
Best Local Similarity 35.0%; Pred. No. 1.5;
Matches 21; Conservative 12; Mismatches 23; Indels 4; Gaps 3;

QY 35 GAATTGNSCTCRDSDGTDSDVDTQCOQAENS AVPTA-DTRSQ-PRDP--VRPGRGPR 90
Db 29 GSOAQGGSCILREARNPHSAGGTAGVGLEAAEPTALLTRAEPPSEPIEIRPKKGP 88

RESULT 6
PCT-US94-07266-2
; Sequence 2, Application PC/TUS9407266
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RESULT 7
US-09-418-710-69
; Sequence 69, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JF98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 1525
; TYPE: PrT
; ORGANISM: Homo sapiens
US-09-418-710-69

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1 FILING DATE:
2 CLASSIFICATION: 435
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Chan, Albert Wai-Kit
5 REGISTRATION NUMBER: 36,479
6 REFERENCE/DOCKET NUMBER: 50288-A
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (212) 278-0400
9 TELEFAX: (212) 391-0525
10 INFORMATION FOR SEQ ID NO. 2:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 462 amino acids
13 TYPE: amino acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16 MOLECULE TYPE: protein
17 US-08-865-537A-2
18
19 Query Match 12.2%; Score 74.5; DB 2; Length 462;
20 Best Local Similarity 29.2%; Pred. No. 1.9;
21 Matches 21; Conservative 10; Mismatches 36; Indels 5; Gaps 1;
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23 QY 12 SRSLGQGLLLTLEEHIAHFLGTGGATTMGNSCICRDDSVDTSVDTQQQAENSAVPTA 71
24 DB 328 SRLSDGTAAGIKKCIDAFAGTGPAPTTSST-----PEASTAPASTTPQTPEDTLVPT 382
25
26 QY 72 DTRSQRPDRVRP 83
27 DB 383 STPAPGPAPTAP 394
28
29 RESULT 9
30 US-08-149-037D-35
31 ; Sequence 35, Application US/08149097D
32 ; Patent No. 5874236
33 ; GENERAL INFORMATION:
34 ; APPLICANT: Harpold, Michael

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; ; OTHER INFORMATION: /product= "Alpha1A-1 subunit of
; ; OTHER INFORMATION: human calcium channel"
; ; US-08-149-097D-35

Query Match 12.1%; Score 73.5; DB 2; Length 2509;
Best Local Similarity 24.2%; Pred. No. 23;
Matches 31; Conservative 9; Mismatches 39; Indels 49; Gaps 4;

QY 12 SRISGGLLLTLEEHIAHFLGTGG-----AATTGNSC----- 44
Ddb 2251 SRPSPG-----REHWAHQGSSVSGSPAFSTGTPRRGRQLQPTSTPRPHVYS 2305
QY 45 -ICRDSGTDDSDYDQOQQAENSAY-----PTADTRSQRPDPVRRPGR 87
Ddb 2306 PVIRKAGSGPPQQOQQOQQOQAVARPGRAATSPRRYPGPTAEPLAGRPPTGGHSG 2365
QY 88 RGPHEPR 95
Ddb 2366 RSPMR 2373

RESULT 10
US-09-029-348-3
; Sequence 3, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
; TITLE OF INVENTION: NOVEL PROCOLLAGENS
; FILE REFERENCE: G087857PUS LISTING
; CURRENT APPLICATION NUMBER: US/09/029,348
; CURRENT FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE
; OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS
US-09-029-348-3

Query Match 12.0%; Score 73; DB 3; Length 623;
Best Local Similarity 28.8%; Pred. No. 4.2;
Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7;

QY 16 GQGLLTLLEEH---IAHFLGTGGAATTGNNS-----CICRDSGT---DDS 55
Ddb 8 GSWLLALLHPTILLAQAEVGGCSHLGQSVADRDVWKPEQCICVC--DSGSLCDDI 65
QY 56 V-DTQOQQAENSAPV-----TADTRSQRPDPVRRPGRGHEPR 94
Ddb 66 ICDDQELDCNPEIFPGECCAVCPQPTAPTRPP-NGQGGQGPX 108

RESULT 11
US-09-029-348-2
; Sequence 2, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
; TITLE OF INVENTION: NOVEL PROCOLLAGENS
; FILE REFERENCE: G087857PUS LISTING
; CURRENT APPLICATION NUMBER: US/09/029,348
; CURRENT FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE

```

; OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS
US-09-029-348-2

Query Match 12.0%; Score 73; DB 3; Length 626;
Best Local Similarity 28.8%; Pred. No. 4.2; Mismatches 36; Indels 28; Gaps 7;
Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7;
QY 16 GQGLLLTLEH---IAHFLGTGGAATTMGNS-----CICRDSGT---DDS 55
DB 8 GSWLLALLHPTIILAQQAEVGGCSHLGQSYADRDVWKPEPCQICVC--DSGVLCDI 65
QY 56 V-DTQOQQAENSVP-----TADTRSQRPDPVPRPRRGPHPR 94
DB 66 ICDDQELDCNPEIPFGCCAVCPPTAPTTRPP-NGQPGQPK 108

RESULT 12

US-09-252-991A-28443
; Sequence 28443, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 28443

; LENGTH: 333

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-28443

Query Match 11.9%; Score 72.5; DB 4; Length 333;
Best Local Similarity 27.5%; Pred. No. 2.1; Mismatches 35; Gaps 3;
Matches 25; Conservative 7; Mismatches 35; Gaps 3;
QY 29 HFLGTGGAATTMGNSCICRDSGTSDSDVTQOQQAENSVP-----TADTRSQRPDPVR 82
DB 216 HRLATGG-----DEGADEGRHHQPRQAAHRRRFLPCPDAGHRRRGAEPR 262
QY 83 P-----PRCRGPHPRKK 97
DB 263 QRTGDPAGHREAPGSLRPRRPRGHLPRRR 293

RESULT 13

US-09-252-991A-20178

; Sequence 20178, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 20178

; LENGTH: 562

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20178

Query Match 11.7%; Score 71.5; DB 4; Length 562;
Best Local Similarity 29.7%; Pred. No. 5.5; Mismatches 22; Conservative 6; Mismatches 29; Indels 17; Gaps 2;
QY 36 AATTMGNSCICRDSGTSDSDVTQOQQAENSVPADTRSQRPDPVPRPRRGPHPR-- 93
DB 79 AATPAG-----EDGQLHQRPRRLAGPGSGAGAPADPRFRRRRGAQRPPP 127
QY 94 ----RRKKQNVDEL 103
DB 128 VAGSRARRSGTDAL 141

RESULT 14

US-09-252-991A-18531

; Sequence 18531, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 18531

; LENGTH: 566

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18531

Query Match 11.7%; Score 71.5; DB 4; Length 566;
Best Local Similarity 23.6%; Pred. No. 5.6; Mismatches 29; Conservative 10; Mismatches 37; Indels 47; Gaps 4;
QY 23 LEEHTAHLGTGGAATTMGNSC--ICRDSGTSDSDV-----TQOQQAENSVP 71
DB 118 LERRLPFGAGGTATGRRRCQRIVROAPGGRSVDPFGHGGPHQAORRAGSGTEG 177
QY 72 DTRSQRPDP-----VAPRR-----CRGPHPR 95
DB 178 RTTRAPRPGGQLPAGKGQVRQAGDRGGAQLRPSRPAAGTELLHGAARRYR 237
QY 96 KQ 98
DB 238 RQR 240

RESULT 15

US-09-252-991A-26099

; Sequence 26099, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 26099

; LENGTH: 863

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26099

Query Match 11.7%; Score 71; DB 4; Length 863;
 Best Local Similarity 29.1%; Fred. No. 11;
 Matches 25; Conservative 8; Mismatches 33; Indels 20; Gaps 3;
 QY 31 LGTGAATT-----MNSICRDSGTDDSYDTQOQAENS AVPTADT-----RS 75
 Db 335 LQPGTAARRTHRPWPGRGAGGDALLRPDAGQADRLRGDPRESPAQADPRAGALRAAGRR 394
 QY 76 QPRDPVRPP-----RRGRGPHEPRK 96
 Db 395 QPAVERQPPGASGLRRRRGDHRLHRR 420

Search completed: April 2, 2004, 10:31:41
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:26:40 ; Search time 39 seconds
(without alignments)
946.555 Million cell updates/sec

Title: US-10-002-796-9

Perfect score: 609

Sequence: 1 MIVFGNAFLASRLQGLL.....QNVGVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriopl.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	604	99.2	576	4	Q96DX4
2	586	96.2	576	6	Q95LP3
3	561	92.1	117	11	Q8BLS8
4	556	91.3	576	11	Q8C039
5	556	91.3	576	11	Q8BVR6
6	86	14.1	601	16	Q82F17
7	85.5	14.0	290	5	Q20394
8	79.5	13.1	356	10	Q9ATR4
9	79.5	13.1	388	10	Q94IM8
10	79.5	13.1	388	10	Q8LN68
11	79.5	13.1	388	10	Q7YIX7
12	79.5	13.1	5146	5	Q9VXR3
13	79	13.0	970	10	Q9AYF2
14	79	13.0	970	10	Q7XF23
15	78.5	12.9	188	2	Q7WX07
16	78	12.8	179	5	Q9XZ40

17	78	12.8	191	5	Q9U0C1
18	78	12.8	480	5	Q9U0C0
19	78	12.8	480	5	Q27033
20	77.5	12.7	550	12	O40912
21	77.5	12.7	550	12	P88903
22	76.5	12.6	634	4	Q8IXW0
23	76	12.5	1063	16	Q8XXH5
24	75.5	12.4	948	5	Q9U304
25	75	12.3	147	5	O15805
26	75	12.3	183	5	Q9U0B5
27	75	12.3	183	5	Q9U0B6
28	75	12.3	204	5	Q9U0B4
29	75	12.3	260	5	Q8IT83
30	75	12.3	267	13	Q9PUV0
31	75	12.3	278	5	Q25862
32	75	12.3	291	5	Q25789
33	74.5	12.2	121	12	Q8QRK4
34	74.5	12.2	462	3	O42721
35	74.5	12.2	2120	5	O8IAK1
36	74	12.2	850	16	Q8FML9
37	73.5	12.1	416	12	Q81265
38	73	12.0	206	5	Q9U0C3
39	73	12.0	220	5	Q9U0B3
40	73	12.0	222	5	Q9U0B1
41	73	12.0	353	11	Q62313
42	73	12.0	579	2	Q8GPF2
43	73	12.0	1160	5	Q8T0V9
44	73	12.0	1163	4	Q8N6U4
45	73	12.0	3571	10	Q9SL27

ALIGNMENTS

RESULT 1

Q96DX4 PRELIMINARY; PRT; 576 AA.

AC Q96DX4; 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein KIAA1972.
 GN KIAA1972.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21842142; PubMed=11853319;
 RA Nagase T., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XXII.
 RT The complete sequences of 50 new cDNA clones which code for large
 proteins."

RT DNA Res. 8:319-327(2001).
 RL EMBL; BC013173; AAH13173.1; -
 DR EMBL; AB075852; BAB85558.1; -
 DR EMBL; AB075852; BAB85558.1; -
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR008938; ARM.
 DR Pfam; PF00622; SPRY; 1.
 DR SMART; SM00184; RING; 1.
 DR SMART; SM00449; SPRY; 1.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Hypothetical protein_ZF_RING_2; 1.
 SQ SEQUENCE 576 AA; 64180 MW; 8598E43E56691F9B CRC64;


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Query Match 99.2%; Score 604; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.2e-57;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
QY 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116
DB 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116

RESULT 2
Q95LP3 PRELIMINARY; PRT; 576 AA.
AC Q95LP3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RA Terao K., Sugano S.;
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA
RT libraries."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB072745; BAB69714.1; -.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 64259 MW; 68D230ADIC4F5F8D CRC64;

Query Match 96.2%; Score 586; DB 6; Length 576;
Best Local Similarity 97.4%; Pred. No. 1.1e-55;
Matches 113; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
QY 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116
DB 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116

RESULT 3
Q8BLS8 PRELIMINARY; PRT; 117 AA.
AC Q8BLS8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical Spla and the Ryanodine receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;

Query Match 99.2%; Score 604; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.2e-57;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
QY 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116
DB 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116

RESULT 2
Q95LP3 PRELIMINARY; PRT; 576 AA.
AC Q95LP3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RA Terao K., Sugano S.;
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA
RT libraries."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB072745; BAB69714.1; -.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 64259 MW; 68D230ADIC4F5F8D CRC64;

Query Match 96.2%; Score 586; DB 6; Length 576;
Best Local Similarity 97.4%; Pred. No. 1.1e-55;
Matches 113; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
QY 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116
DB 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116

RESULT 3
Q8BLS8 PRELIMINARY; PRT; 117 AA.
AC Q8BLS8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical Spla and the Ryanodine receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
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```
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RL EMBL; AK043522; BAC31566.1; -.
KW Hypothetical protein.
SQ SEQUENCE 117 AA; 12738 MW; D3FEC471ABD55D3C CRC64;

Query Match 92.1%; Score 561; DB 11; Length 117;
Best Local Similarity 91.5%; Pred. No. 9.5e-54;
Matches 107; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGAEDNVDTHQ 60
QY 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVDK 117
DB 61 QOAENSTVTDTSRQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVDK 117

RESULT 4
Q8C039 PRELIMINARY; PRT; 576 AA.
AC Q8C039;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical Spla and the Ryanodine receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RL EMBL; AK032416; BAC27858.1; -.
DR MGD; MGI:1914860; 4930470D19Rik.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 64340 MW; D72D60E803911D02 CRC64;

Query Match 91.3%; Score 556; DB 11; Length 576;
Best Local Similarity 91.4%; Pred. No. 2.2e-52;
Matches 106; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGAEDNVDTHQ 60
QY 61 QOAENSAPTADTRSQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116
DB 61 QOAENSTVTDTSRQPRDPVPPRRGRGPHPRKKNQVGLVLDTLAVIRTLVD 116

RESULT 5
Q8BVR6 PRELIMINARY; PRT; 576 AA.
ID Q8BVR6
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AC Q8BVR6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical Spla and the Ryanodine receptor (Hypothetical
DE protein)
DE 430470D19RIK.
GN Mus musculus (Mouse)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=2234683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC STRAIN=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Besak S.A., McQuellan J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra W.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK076799; BAC36485.1; -
DR EMBL; BC054121; AAH54121.1; -
DR MGD; MGI:1914860; 4930470D19RIK.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR001841; Znf_Fing.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 64322 MW; 823C3532FCE18387 CRC64;

Query Match 91.3%; Score 556; DB 11; Length 576;
Best Local Similarity 91.4%; Pred. No. 2.2e-52;
Matches 106; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIVFGWVFLASRLSGGLLTLEHIAHFLGTGGAATTWNSICIRDDSGTSDSDVDTQ 60
DB 1 MIVFGWVFLASRLSGGLLTLEHIAHFLGTGGAATTWNSICIRDDSGAENVDVTHQ 60

QY 61 QQAENSAPTADTSQRDPVPRPRRGKGPHEPRKKQNVGDLVLDTLAVIRLVD 116
DB 61 QQAENSTVPTDSRSPRDPVPRPRRGKGPHEPRKKQNVGDLVLDTLAVIRLVD 116

RESULT 6
Q82FI7
ID Q82FI7 PRELIMINARY; PRT; 601 AA.
AC Q82FI7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative chitamine biosynthesis protein.
GN THIA OR SAV4265.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
CX NCBI_TaxID=33903;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005038; BAC71977.1; -
DR GO; GO:0009228; B:thiamin biosynthesis; IEA.
DR InterPro; IPR002817; Thic.
DR Pfam; PF01964; Thic; 1.
DR ProDom; PD007048; Thic; 1.
DR TIGRFAMs; TIGR00190; thic; 1.
KW Complete proteome.
SQ SEQUENCE 601 AA; 66485 MW; B149CD75A602FCF5 CRC64;

Query Match 14.1%; Score 86; DB 16; Length 601;
Best Local Similarity 32.3%; Pred. No. 0.86;
Matches 31; Conservative 7; Mismatches 36; Indels 22; Gaps 4;

QY 39 TWGNSCICRDDSG--TDDSVPTQQQA-----ENSAVPTADTSQRDPVPRP----- 83
DB 55 TWGNSVTLTDSGPTDFSVTDVVRGLAPRENWIIARGTTEEVAGRFVPEDDGDKHT 114

QY 84 -PRRGK-----PHEPRKKQNVGDLVLDTLAVIR 112
DB 115 SPRGGLRLNLDVAFVPRGRPRGRGRDQAVTQLAVAR 150

RESULT 7
Q20394
ID Q20394 PRELIMINARY; PRT; 290 AA.
AC Q20394;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F44D12.6 protein.
GN F44D12.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RP Coles L.;

```
RL Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
   investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z68298; CAA92602.1; -.
DR PIR; T22161; T22161
DR WormPep; F44D12.6; CE03330.
DR SEQUENCE 290 AA; 32831 MW; B60BEFE9C89E7780 CRC64;

Query Match
Best Local Similarity 14.0%; Score 85.5; DB 5; Length 290;
Matches 27; Conservative 15; Mismatches 31; Indels 17; Gaps 5;

QY 24 EBHIAHFLGTGAATMGN-SCICRDSGTD-----DSVDTQQQQAENSAVPTADTSQP 77
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
154 DAHV-HWRETGLAFIRSDACRSKDDGCDTIDSKNSKEDQERSKYNSEMPLESD----- 207
QY 78 RDPVPRPRGRGPHPRKKNVGLVLDLT 107
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
208 KPDRKPKQ-----EPRRSKQRTGPMPT 232

RESULT 8
Q9ATR4
ID Q9ATR4 PRELIMINARY; PRT; 356 AA.
AC Q9ATR4;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Teosinte branched protein (Fragment).
GN TBI.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21165336; PubMed=11264415;
RA Lukens L., Doebley J.;
RT "Molecular evolution of the teosinte branched gene among maize and
   related grasses."
RL Mol. Biol. Evol. 18:627-638(2001).
DR EMBL; AF322143; AAK37505.1; -.
DR Gramene; Q9ATR4; -.
DR InterPro; IPR005333; TCP.
DR Pfam; PF03634; TCP; 1.
FT NON_TER 1
FT NON_TER 356
SQ SEQUENCE 356 AA; 37757 MW; 95D7174BC6A8BF84 CRC64;

Query Match
Best Local Similarity 13.1%; Score 79.5; DB 10; Length 356;
Matches 20; Conservative 6; Mismatches 27; Indels 9; Gaps 1;

QY 43 SCICRDSGTDSDVDTQQQQAENSA-----VPTADTSQPRDPVPRRGRGPHEP 93
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
180 SSVCEEDGSSLSVDGKQOQHNPADRGAGDHGKGAHGHSDGKPAKPRRAAANPKPP 239
QY 94 RR 95
DB 240 RR 241

RESULT 9
Q941M8
ID Q941M8 PRELIMINARY; PRT; 388 AA.
AC Q941M8;
DT 01-DEC-2001 (TREMELrel. 19, Created)
```

Query Match 13.1% Score 79.5; DB 10; Length 388;
 Best Local Similarity 32.3%; Pred. No. 2.7;
 Matches 20; Conservative 6; Mismatches 27; Indels 9; Gaps 1;

QY 43 SCICRDSGTDSDVDTQQAENSA-----VPTADTRSPDPVPRGRGPHEP 93
 Db 179 SSVCEEDGSSLSVDGKQOQHSNPDARGGAGDHKGAAHGHSCKKPAKPRRAAANKPP 238

QY 94 RR 95
 Db 239 RR 240

RESULT 11

QY1X7 PRELIMINARY; PRT; 388 AA.

AC QY1X7
 DT 01-OCT-2003 (TEMBLrel. 25, Created)
 DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Teosinte-branching 1.
 GN TBL.
 OS Oryza sativa (indica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=39946;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. IR-36;
 RC Hu W., Zhang S., Zhao Z., Zhao Y., Sun C.R., Luo D.,
 RT "The structural and expression analysis of OsTb1 in rice."
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY286002; AAB37176.1;
 SQ SEQUENCE 388 AA; 41504 MW; 8CF363D2EAA02743 CRC64;

Query Match 13.1% Score 79.5; DB 10; Length 388;
 Best Local Similarity 32.3%; Pred. No. 2.7;
 Matches 20; Conservative 6; Mismatches 27; Indels 9; Gaps 1;

QY 43 SCICRDSGTDSDVDTQQAENSA-----VPTADTRSPDPVPRGRGPHEP 93
 Db 179 SSVCEEDGSSLSVDGKQOQHSNPDARGGAGDHKGAAHGHSCKKPAKPRRAAANKPP 238

QY 94 RR 95
 Db 239 RR 240

RESULT 12

Q9VXR3 PRELIMINARY; PRT; 5146 AA.

AC Q9VXR3
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE C8184 protein.
 GN C8184.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasearman D.A., Weinstein G.M., Weissenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*."
 Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banton J., An H., Baldwin D., Banton J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorset V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jalili M., Kruse D., Li P., Mattei B., Moshrefi A., Nunco J.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Pacleb J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouaneavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svitskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 "Sequencing of *Drosophila melanogaster* genome."
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Ruso S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 "Annotation of *Drosophila melanogaster* genome."
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celnik S.E., Gibb R.A., Rubin G.M., Venter C.J.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003500; AAF48495.2;
 DR FlyBase: FBgn0030674; CG8184.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO: GO:0005488; F:binding; IEA.

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DR GO: 0004842; Fubiquitin-protein ligase activity; IEA.
DR GO: 0006810; P-transport; IEA.
DR GO: 0006512; P-biquitin cycle; IEA.
DR InterPro: IPR008938; ARM.
DR InterPro: IPR000569; HECT domain.
DR InterPro: IPR001993; Mitoch. carrier.
DR InterPro: IPR000449; UBA domain.
DR Pfam: PF00632; HECT; 1.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF02825; WVE; 1.
DR SMART: SM00119; HECTC; 1.
DR PROSITE: PS0237; HECT; 1.
DR PROSITE: PS00215; MITOCH. CARRIER; 1.
DR PROSITE: PS00310; UBA; 1.
SQ SEQUENCE 5146 AA; 56847 MW; 27BF187F2D279846 CRC64;

Query Match 13.1%; Score 79.5; DB 5; Length 5146;
Best Local Similarity 30.1%; Pred. No. 54;
Matches 22; Conservative 8; Mismatches 30; Indels 13; Gaps 2;

QY 32 GTGGAATTGNSCICRDSGTDSDVDTQQAENS AVPTADTRSQPRDPVPRRGGRPH 91
DB 853 GTGSASSVQLGAADTNDSDGDDDDDDSSA-----SQQQQPTTPGGGGPS 901

QY 92 EPRKKQNVGLV 104
DB 902 TPR--TQAGGV 912

RESULT 13
ID Q9AYF2 PRELIMINARY; PRT; 970 AA.
AC Q9AYF2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Zea mays chromosome 422kDazein-associated intercluster
DE region, copia-type polypolyprotein.
GN OSJNBA0094J09.18.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RT "Genomic Sequence For Oryza sativa, Nipponbare strain, Chromosome X,
RT Clone OSJNBA0094J09, complete sequence.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA McCombie W.R.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA McCombie W.R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bal H.P., See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
RA Preston R.R., Huang E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
RA Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; ACU78839; AAK13102.1; -.
DR Gramene; Q9AYF2; -.
DR GO: 0003677; F:DNA binding; IEA.
DR GO: 0004289; F:subtilase activity; IEA.

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DR GO: 0006310; P:DNA recombination; IEA.
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000209; Peptidase_S8.
DR InterPro: IPR001584; Rve.
DR Pfam: PF00665; Rve; 1.
DR PROSITE: PS00136; SUBTILASE ASP; 1.
SQ SEQUENCE 970 AA; 108499 MW; 14D8F3EB056B194A CRC64;

Query Match 13.0%; Score 79; DB 10; Length 970;
Best Local Similarity 27.4%; Pred. No. 8.8;
Matches 31; Conservative 12; Mismatches 42; Indels 28; Gaps 6;

QY 4 FGWAVFLASRLG-----QGLLTLEHIAHFICT-----GGAATTM--GNSCICRDP 49
DB 551 YSWVFFMATKDEAFQHFRGLFLRD---LEFPGLKRIKSDNGTUSQVGEDSCIFEDD 607

QY 50 SGTDDSDVDTQQAENS AVPTADTRSQPRDPVPRRGGRPHPRKKQNVG 102
DB 608 SDDDDKVGSGAGTGRAGQTAST-----PP--GRPPQDERSNRPGSSG 649

RESULT 14
ID Q7XF23 PRELIMINARY; PRT; 970 AA.
AC Q7XF23;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Zea mays chromosome 422kDazein-associated intercluster
DE region, copia-type polypolyprotein.
GN OSJNBA0094J09.18.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RA "In-depth view of structure, activity, and evolution of rice
RA chromosome 10.";
RL Science 300:1566-1569 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017089; AAP53536.1; -.
RW Polyprotein.
SQ SEQUENCE 970 AA; 108499 MW; 14D8F3EB056B194A CRC64;

Query Match 13.0%; Score 79; DB 10; Length 970;
Best Local Similarity 27.4%; Pred. No. 8.8;
Matches 31; Conservative 12; Mismatches 42; Indels 28; Gaps 6;

QY 4 FGWAVFLASRLG-----QGLLTLEHIAHFICT-----GGAATTM--GNSCICRDP 49
DB 551 YSWVFFMATKDEAFQHFRGLFLRD---LEFPGLKRIKSDNGTUSQVGEDSCIFEDD 607

QY 50 SGTDDSDVDTQQAENS AVPTADTRSQPRDPVPRRGGRPHPRKKQNVG 102
DB 608 SDDDDKVGSGAGTGRAGQTAST-----PP--GRPPQDERSNRPGSSG 649

RESULT 15
ID Q7WX07 PRELIMINARY; PRT; 188 AA.
AC Q7WX07;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative single-strand binding protein.

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GN SSB OR PHG335.
 OS Alcalligenes eutrophus (Ralstonia eutropha).
 OG Plasmid megaplasmid phG1.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=510;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=H16;
 RC Schwartz E., Henne A., Cramm R., Eitinger T., Friedrich B.,
 RA Gottschalk G.;
 RT "Complete Nucleotide Sequence of phG1: A Ralstonia eutropha H16
 RT Megaplasmid Encoding Key Enzymes Of H2-based Lithoautotrophy and
 RT Anaerobiosis";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY305378; AAF86084.1; -.
 KW Plasmid.
 SQ SEQUENCE 188 AA; 20451 MW; B43832FBCC232CF4 CRC64;
 Query Match 12.9%; Score 78.5; DB 2; Length 188;
 Best Local Similarity 33.8%; Pred No. 1.5; Mismatches 13; Gaps 5;
 Matches 26; Conservative 8; Indels 30; Indels 13; Gaps 5;
 Qy 32 GTGGAATTMGNSCICRDDSGTDSVDTQQQAENSAYPTADTSQP--RDPVPPRRGRG 89
 Db 110 GRCASD--GDS-----DSGTDRSASQSPASQRSAPTGG-RQPPARRQPAQPPSNGFG 161
 Qy 90 PHE---PRKKQNVGL 103
 Db 162 DFNEDIFARPALDGI 178

Search completed: April 2, 2004, 10:30:33
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:26:10 ; Search time 17 Seconds
(without alignments)
358.365 Million cell updates/sec

Title: US-10-002-796-9

Perfect score: 609

Sequence: 1 MIVFGWVFLASRLSQGLL.....QNVGVLDTLAVITLVDK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	13.0	612	1	THIC_STRCO
2	78.5	12.9	188	1	SSB_ALCEU
3	78	12.8	1483	1	BALB_HUMAN
4	75	12.3	286	1	MSA2_PLAF1
5	73.5	12.1	2505	1	CCAA_HUMAN
6	73	12.0	281	1	MSA2_PLAFH
7	73	12.0	353	1	TGNI_MOUSE
8	73	12.0	1466	1	CAL3_HUMAN
9	72.5	11.9	282	1	MSA2_PLAF2
10	72.5	11.9	272	1	MSA2_PLAF7
11	72.5	11.9	274	1	MSA2_PLAF6
12	72.5	11.9	287	1	MSA2_PLAF3
13	72.5	11.9	300	1	MSA2_PLAF1
14	72.5	11.9	300	1	MSA2_PLAF2
15	72.5	11.9	302	1	MSA2_PLAF9
16	72.5	11.9	347	1	MSA2_PLAF2
17	72.5	11.9	458	1	YNE1_CABEL
18	72	11.8	1787	1	CHD3_CABEL
19	71	11.7	1479	1	BALB_MOUSE
20	70.5	11.6	3726	1	TRX_DROME
21	70	11.5	445	1	NRH3_MOUSE
22	69	11.3	1944	1	CHD3_HUMAN
23	68	11.2	424	1	COT1_BOVIN
24	68	11.2	445	1	NRH3_RAT
25	68	11.2	504	1	FTSY_SSNY3
26	68	11.2	702	1	EXO1_YEAST
27	67.5	11.1	399	1	SIR3_HUMAN
28	67.5	11.1	727	1	CTCF_HUMAN
29	67.5	11.1	1298	1	ICP4_HSV1
30	67	11.0	393	1	CIM4_HUMAN
31	67	11.0	1202	1	NOS3_HUMAN
32	67	11.0	3828	1	TRX_DROVI
33	66.5	10.9	217	1	YKR4_EBV

ALIGNMENTS

RESULT 1

```

THIC_STRCO
ID THIC_STRCO STANDARD; PRT; 612 AA.
AC Q9X9U0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thiamine biosynthesis protein thic.
GN THIC OR SCO3928 OR SCQ11.11.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_taxid=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovich E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RA "Complete genome sequence of the model actinomycete Streptomyces
RA coelicolor A3(2).";
RT Nature 417:141-147(2002).
RL
CC -!- FUNCTION: Required for the synthesis of the hydromethylpyrimidine
CC (HMP) moiety of thiamine (4-amino-2-methyl-5-
CC hydroxymethylpyrimidine) (By similarity).
CC -!- PATHWAY: Thiamine biosynthesis.
CC -!- SIMILARITY: Belongs to the thic family.
CC
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CC
CC EMBL; AL939118; CAB46966.1; -.
DR PIR; T37181; T37181.
DR HANAP; MF_00089; -.
DR InterPro; IPR002817; Thic.
DR Pfam; PF01964; thic; 1.
DR ProDom; PD007048; Thic; 1.
DR TIGRFAMs; TIGR00190; thic; 1.
KW Thiamine biosynthesis; Complete proteome.
SQ
SEQUENCE 612 AA; 67371 MW; 230BF254200CF68 CRC64;

```

Query Match 13.0%; Score 79; DB 1; Length 612;
Best Local Similarity 31.2%; Pred. No. 2.4;
Matches 30; Conservative 7; Mismatches 37; Indels 22; Gaps 4;

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QY 39 TWGNSICRDSG--TDSVDTQOQA-----ENSAVTATRSQPRDPVNP----- 83
DB 60 TNGQSVTLTYDTSGPYTDLVDTRVGLAPLRENWIIARGDTEEVAGRPVPEPDGKHT 119
QY 84 -PRRGSG-----PHEPRKKNQVGLVLDLTGLAVR 112
DB 120 SPRGGRLNLDVFPGRPRQPRGRDGNVQLAYAR 155

RESULT 2
SSB ALCEU
ID SSB ALCEU STANDARD; PRT; 188 AA.
AC P5927: Q7WX07;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Single-strand binding protein (SSB) (Helix-stabilizing protein).
GN SSB OR PHG335.
OS Algaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H16 / DSM 428 / ATCC 17699;
RA Schwartz E., Henne A., Cramm R., Eitinger T., Friedrich B.,
RA Gottschalk G.;
RT "Complete nucleotide sequence of pHG1: a Ralstonia eutropha H16
RT megaplasmid encoding key enzymes of H2-based lithoautotrophy and
RT anaerobiosis.";
RL J. Mol. Biol. 332:369-383(2003).
CC -!- FUNCTION: This protein is essential for replication of the
CC chromosome. It is also involved in DNA recombination and repair
CC (By similarity).
CC -!- SIMILARITY: Contains 1 SSB domain.
CC
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CC
CC EMBL; AY305378; AAP86084.1; -
CC PROSITE; P550935; SSB: 1.
CC DNA-binding; DNA repair; DNA replication; Plasmid.
FT DOMAIN 4 109
SQ SEQUENCE 188 AA; 20451 MW; E43832FBC232CF4 CRC64;

Query Match 12.9%; Score 78.5; DB 1; Length 188;
Best Local Similarity 33.8%; Pred. No. 0.71;
Matches 26; Conservative 8; Mismatches 30; Indels 13; Gaps 5;

QY 32 GTGGATATGNSICRDSGTDSDVDTQOQAENSAVTATRSQ--RDPVPRRGSG 89
DB 110 GRGGASD--GDS-----DSGTRDSAQSPASQAQSAPTQ--RQPPARRQAPPPSNGFG 161
QY 90 PHE---PRRKQNVGL 103
DB 162 DFNEIDIPARPAALDGI 178

RESULT 3
BA1B HUMAN
ID BA1B HUMAN STANDARD; PRT; 1483 AA.
AC Q9UIG0; O95039; O95247; O95277;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bromodomain adjacent to zinc finger domain protein 1B (Williams-Beuren

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DE syndrome chromosome region 9 protein) (WBSR9) (Williams syndrome
DE transcription factor) (HWALE2).
GN BAZ1B OR WBSR9 OR WBSR10 OR WSTF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=9907764; PubMed=9858827;
RA Peoples R.J., Cisco M.J., Kaplan P., Francke U.;
RT "Identification of the WBSR9 gene, encoding a novel transcriptional
RT regulator, in the Williams-Beuren syndrome deletion at 7q11.23.";
RL Cytogenet. Cell Genet. 82:238-246(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99047530; PubMed=9828126;
RA Lu X., Meng X., Morris C.A., Keating M.T.;
RT "A novel human gene, WSTF, is deleted in Williams Syndrome.";
RL Genomics 54:241-249(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RX MEDLINE=20130112; PubMed=10662543;
RA Jones M.H., Hamana N., Nezu J., Shimane M.;
RT "A novel family of bromodomain genes.";
RL Genomics 63:40-45(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Minx P., Graves T., Duckels G., Harrison M., Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=21977304; PubMed=11980720;
RA Bozhenok L., Wade P.A., Varga-Weisz P.;
RT "WSTF-ISWI chromatin remodeling complex targets heterochromatic
RL replication foci.";
RN EMBL J. 21:2231-2241(2002).
CC -!- FUNCTION: Forms a chromatin remodeling complex that mobilizes
CC nucleosomes and reconfigures irregular chromatin to a regular
CC nucleosomal array structure.
CC -!- SUBUNIT: Interacts with ISWI (imitation SWI protein) to form the
CC WSTF-ISWI chromatin remodeling complex (WICH).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential). Accumulates in
CC pericentromeric heterochromatin during replication.
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UIG0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UIG0-2; Sequence=VSP_000552;
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed with high levels of
CC expression in heart, brain, placenta, skeletal muscle and ovary.
CC -!- DEVELOPMENTAL STAGE: Expressed at equal levels in 19-23 weeks old
CC fetal tissues.
CC -!- DISEASE: Haploinsufficiency of BAZ1B may be the cause of certain
CC cardiovascular and musculo-skeletal abnormalities observed in
CC Williams-Beuren syndrome (WBS), a rare developmental disorder. It
CC is a contiguous gene deletion syndrome involving genes from
CC chromosome band 7q11.23.
CC -!- SIMILARITY: Belongs to the WAL family.
CC -!- SIMILARITY: Contains 1 bromodomain.
CC -!- SIMILARITY: Contains 1 DDT domain.
CC -!- SIMILARITY: Contains 1 PHD-type zinc finger.
CC -!- SIMILARITY: Contains 1 WAC domain.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
CC in positions 1031, 1042 and 1422.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to a
CC frameshift in position 1478.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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DR EMBL; AF084479; AAD08675.1; -;
DR EMBL; AF072810; AAC97879.1; ALT FRAME.
DR EMBL; AB032253; BAA89210.1; ALT FRAME.
DR EMBL; AC005074; AAD04720.1; ALT SEQ.
DR EMBL; AC005089; -; NOT_ANNOTATED_CDS.
DR HSP; O22831; 1391.
DR TRANSFAC; T04145; -;
DR Genew; HGNC:961; BAZ1B.
DR MIN; 605681; -;
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003700; F:transcription factor activity; NAS.
DR GO; GO:0008270; F:zinc ion binding; NAS.
DR GO; GO:0006350; P:transcription; NAS.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR004022; DDT_dom.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00439; bromodomain; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00237; BROMO; 1.
DR SMART; SM00571; DDT; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
DR PROSITE; PS0014; BROMODOMAIN_2; 1.
DR PROSITE; PS08027; DDT; 1.
DR PROSITE; PS01359; ZF_PHD_1; 1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
KW Transcription regulation; Bromodomain; Zinc-finger; Coiled coil;
KW Nuclear protein; Alternative splicing; Williams-Beuren syndrome.
FT DOMAIN 20 126
FT DOMAIN 604 668
FT ZN_FING 1184 1234 PHD-TYPE.
FT DOMAIN 1356 1426 BROMODOMAIN.
FT DOMAIN 306 578 LYS-RICH
FT DOMAIN 533 586 COILED COIL (POTENTIAL).
FT DOMAIN 768 814 COILED COIL (POTENTIAL).
FT DOMAIN 850 893 COILED COIL (POTENTIAL).
FT DOMAIN 1245 1283 COILED COIL (POTENTIAL).
FT DOMAIN 1261 1273 POLY-GLU.
FT VARSPIC 560 563 Missing (in isoform 2).
FT CONFLICT 14 14 /Ptd-5p 000552.
FT CONFLICT 22 22 K -> N (IN REF. 3).
FT CONFLICT 136 136 L -> F (IN REF. 3).
FT CONFLICT 191 191 K -> E (IN REF. 1).
FT CONFLICT 298 298 N -> D (IN REF. 4).
FT CONFLICT 823 823 Y -> V (IN REF. 4).
FT CONFLICT 823 823 E -> R (IN REF. 3).
FT CONFLICT 1191 1191 R -> P (IN REF. 2).
FT CONFLICT 1354 1354 K -> M (IN REF. 3).
FT CONFLICT 1438 1438 A -> V (IN REF. 3).
SQ SEQUENCE 1483 AA; 170902 MW; 0CC146FEB954261 CRC64;

Query Match 12.8%; Score 78; DB 1; Length 1483;
Best Local Similarity 27.5%; Pred. No. 8;
Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;

QY 48 DSGTDSVDTQQQAENSVAFTADTRSPQDPVR-----PP-----RRGQFHPRR 95
Db 1255 EDDSDDEEEEDVEVAGLRRLPRKTRGKHSVIPAARGSRPGKPKHSTR 1314
QY 96 KK-----QNVGLVLT 107
Db 1315 SQPKAPPVDDAEVDLVLT 1334

RESULT 4

MSA2_PLAF1 STANDARD; PRT; 286 AA.
ID P50496;
AC P50496;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2).
GN MSA2.
OS Plasmodium falciparum (isolate 311).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN NCBI_TaxID=57265;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9217826; PubMed=1542312;
RA Marshall V.M.; Coppel R.L.; Anders R.F.; Kemp D.J.;
RT "Two novel alleles within subfamilies of the merozoite surface
antigen 2 (MSA-2) of Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 50:181-194(1992).
CC -!- FUNCTION: May play a role in the merozoite attachment to the
erythrocyte.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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DR EMBL; M73809; AAA29697.1; -;
DR InterPro; IPR001136; MSA_2.
DR Pfam; PF00585; MSA_2; 1.
KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW GPI-anchor; Merozoite.
FT SIGNAL 1 20
FT CHAIN 21 262
FT PROPEP 263 286
FT DOMAIN 44 212 POLYMORPHIC REGION.
FT DOMAIN 115 122 POLY-THR.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 286 AA; 28844 MW; D1F4947CE68D5805 CRC64;
Query Match 12.3%; Score 75; DB 1; Length 286;
Best Local Similarity 34.6%; Pred. No. 2.5;
Matches 27; Conservative 6; Mismatches 25; Indels 20; Gaps 5;
QY 32 GTGGA-----ATTMGNSICRDBSDSGTDDSV-----DT-----QQQAENSVAFTADT 73
Db 147 GNGVQKPNQANKETQNNNV-QDSQTSKSNVPPPTQDADTKSPTAQPEQAENSA-PTAEQ 204
QY 74 RSQPRDPVPPRRGRGPH 91
Db 205 TESPELQSAPEKNKGTHQ 222
RESULT 5
CCAA_HUMAN STANDARD; PRT; 2505 AA.
ID CCAA_HUMAN
AC Q00555; P78510; P78511; Q16290; Q92690; Q99790; Q99791; Q99792;
AC Q99793;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Voltage-dependent P/Q-type calcium channel alpha-1A subunit. (Calcium

DE channel, L type, alpha-1 polypeptide isoform 4) (Brain calcium channel
DE 1) (BI).
GN CACNA1A OR CACNA1A4 OR CACNA1A OR CACNA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2).
RC TISSUE=Neuron;
RX MEDLINE=99158614; PubMed=10049321;
RA Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,
RA Harold M.M., Johnson E.C., Williams M.E.;
RT "Structural elements in domain IV that influence biophysical and
RT pharmacological properties of human alpha1A-containing high-voltage-
RT activated calcium channels";
RL Biophys. J. 76:1384-1400(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS PHM.
RC TISSUE=Cerebellum;
RX MEDLINE=97053792; PubMed=8898206;
RA Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J.,
RA Hoffman S.M.G., Lamerdin J.E., Mohrenweiser H.W., Bulman D.E.,
RA Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,
RA Ferrari M.D., Frants R.R.;
RT "Familial hemiplegic migraine and episodic ataxia type-2 are caused by
RT mutations in the Ca_v2.1 channel gene CACNA1A4";
RL Cell 87:543-552(1996).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=97141920; PubMed=8988170;
RA Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,
RA Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;
RT "Autosomal dominant cerebellar ataxia (SCA6) associated with small
RT polyglutamine expansions in the alpha 1A-voltage-dependent calcium
RT channel.";
RL Nat. Genet. 15:62-69(1997).
RN [4]
RP SEQUENCE OF 1233-1651 FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stiilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomerly M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1693-1807 FROM N.A.
RC TISSUE=Lung carcinoma;
RX MEDLINE=95123449; PubMed=7823133;
RA Barry E.L.R., Viglione M.P., Kim Y.I., Froehner S.C.;
RT "Expression and antibody inhibition of P-type calcium channels in
RT human small-cell lung carcinoma cells";
RL J. Neurosci. 15:274-283(1995).
RN [6]
RP SEQUENCE OF 2038-2258 FROM N.A.
RC TISSUE=Frontal cortex;
RX MEDLINE=96102310; PubMed=8525433;
RA Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,
RA McNinis M.G., Ross C.A.;
RT "Characterization of cDNA clones containing CCA trinucleotide repeats
RT derived from human brain.";
RL Somat. Cell Mol. Genet. 21:279-284(1995).
CC -1- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. The isoform alpha-1A
CC gives rise to P and/or Q-type calcium currents. P/Q-type calcium
CC channels belong to the "high-voltage activated" (HVA) group and

are blocked by the funnel toxin (Ftx) and by the omega-agatoxin-
IVA (omega-Aga-IVA). They are however insensitive to
dihydropyridines (DHP), and omega-conotoxin-GVIA (omega-CTX-GVIA).
-1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=7;
Comment=Additional isoforms seem to exist;
Name=BI-1-GCAG; Synonyms=1A-1;
IsoId=000555-1; Sequence=Displayed;
Name=BI-1; Synonyms=1A-2;
IsoId=000555-2; Sequence=VSP_000875;
Name=BI-1(V1);
IsoId=000555-3; Sequence=VSP_000871, VSP_000875;
Name=BI-1(V1)-GCAG;
IsoId=000555-4; Sequence=VSP_000871;
Name=BI-1(V2);
IsoId=000555-5; Sequence=VSP_000872;
Name=BI-1(V2)-GCAG;
IsoId=000555-6; Sequence=VSP_000872;
Name=BI-1(V2 V3);
IsoId=000555-7; Sequence=VSP_000873, VSP_000874;
-1- TISSUE SPECIFICITY: Brain specific; mainly found in cerebellum,
cerebral cortex, thalamus and hypothalamus. No expression in
heart, kidney, liver or muscle. Purkinje cells contain
predominantly P-type VSCC, the Q-type being a prominent calcium
current in cerebellar granule cells.
-1- DOMAIN: Each of the four internal repeats contains five
hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
positively charged transmembrane segment (S4). S4 segments
probably represent the voltage-sensor and are characterized by a
series of positively charged amino acids at every third position.
-1- POLYMORPHISM: The poly-Gln region of CACNA1A is polymorphic: 6 to
17 repeats in the normal population, expanded to about 21 to 30
repeats in spinocerebellar ataxia 6 (SCA6) patients. There seems
to be a correlation between the repeat number and earlier onset of
the disorder.
-1- DISEASE: Defects in CACNA1A are the cause of spinocerebellar
ataxia type 6 (SCA6) [MIM:193086]. SCA6 is an autosomal dominant
disorder characterized by slowly progressive cerebellar ataxia of
the limbs and gait, dysarthria, nystagmus, and mild vibratory and
proprioceptive sensory loss. These symptoms are probably explained
by severe loss of cerebellar Purkinje cells. SCA6 is caused by
expansion of a CAG repeat in the coding region of CACNA1A.
-1- DISEASE: Defects in CACNA1A are the cause of familial hemiplegic
migraine (FHM) [MIM:141500]; also known as migraine familial
hemiplegic 1 (MHP1). FHM, a rare autosomal dominant subtype of
migraine with aura, is associated with ictal hemiparesis and, in
some families, progressive cerebellar atrophy.
-1- DISEASE: Defects in CACNA1A are the cause of episodic ataxia type
2 (EA-2) [MIM:108500]; also known as acetazolamide-responsive
hereditary paroxysmal cerebellar ataxia (APCA). This autosomal
dominant disorder is characterized by acetazolamide-responsive
attacks of cerebellar ataxia and migraine-like symptoms,
interictal nystagmus, and cerebellar atrophy.
-1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
family.

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EMBL; AF004884; AAB61613.1; -.

DR

DR EMBL; AF004883; AAB61612.1; --
 DR EMBL; X98987; CAA68172.1; --
 DR EMBL; Z80114; --; NOT_ANNOTATED_CDS.
 DR EMBL; Z80115; --; NOT_ANNOTATED_CDS.
 DR EMBL; U79665; AAB64179.1; --
 DR EMBL; U79663; AAB49674.1; ALT INIT.
 DR EMBL; U79664; AAB49675.1; ALT INIT.
 DR EMBL; U79665; AAB49676.1; ALT INIT.
 DR EMBL; U79667; AAB49677.1; ALT INIT.
 DR EMBL; U79668; AAB49678.1; ALT INIT.
 DR EMBL; AC005305; AAC26839.1; --
 DR EMBL; S76537; AAB33068.1; --
 DR EMBL; U06702; --; NOT_ANNOTATED_CDS.
 DR Genew; HGNC:1388; CACNALA.
 DR MIM; 601011; --
 DR MIM; 183086; --
 DR MIM; 141500; --
 DR MIM; 108500; --
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002077; Ca_channel_alpha.
 DR InterPro; IPR002111; Cat_channel_TpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M_channel_nlg.
 DR InterPro; IPR005448; PQVDCALPHAI.
 DR Pfam; PF00520; Ion_trans; 4.
 DR PRINTS; PR00167; CACHANNEL.
 DR PRINTS; PR01632; PQVDCALPHAI.
 DR KIC channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;
 KW Disease mutation; Triplet repeat expansion.
 FT REPEAT 85 363
 FT REPEAT 473 717
 FT REPEAT 1231 1514
 FT REPEAT 1551 1814
 FT DOMAIN 1 98
 FT TRANSMEM 99 117
 FT DOMAIN 118 135
 FT TRANSMEM 136 155
 FT DOMAIN 156 167
 FT TRANSMEM 168 185
 FT DOMAIN 186 190
 FT TRANSMEM 191 209
 FT DOMAIN 210 228
 FT TRANSMEM 229 248
 Query Match 12.1%; Score 73.5; DB 1; Length 2505;
 Best Local Similarity 24.2%; Pred. No. 41;
 Matches 31; Conservative 9; Mismatches 39; Indels 49; Gaps 4;
 QY 12 SRSLGQGLLTLEHIAHFLGTGG-----AATTWNSC-----44
 DB 2247 SRSPSEG-----REHMAHQSSSVSGSPAPSTGTPRRGRRLQPLQPTSTPRPHVSYS 2301
 QY 45 -ICRDSGTDSDVTQQQQAENSVA-----PTADTRSPDRPVRPRAG 87
 DB 2302 PVIRKAGSGPPQQQQQQQQQAVRPGRAATGPRRYGPTAEPLAGDRPTGCHSSG 2361
 QY 88 RGPHEPR 95
 DB 2362 RSPRMER 2369
 RESULT 6
 MSA2_PLAFH
 ID MSA2_PLAFH STANDARD; PRT; 281 AA.
 AC Q99319;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 3).

GN MSA2.
 OS Plasmodium falciparum (isolate thtn / Thailand).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=70151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9121803; PubMed=2090943;
 RA Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
 RT "Sequence comparison of allelic forms of the Plasmodium falciparum
 merozoite surface antigen MSA2.";
 RL Mol. Biochem. Parasitol. 43:211-220(1990).
 CC !- FUNCTION: May play a role in the merozoite attachment to the
 CC erythrocyte.
 CC !- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (potential).
 CC !- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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 DR EMBL; M60189; AAA29689.1; --
 DR InterPro; IPR001136; MSA_2.
 DR Pfam; PF00985; MSA_2; 1.
 DR Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
 KW GPI-anchor; Merozoite.
 FT SIGNAL 1 20
 FT CHAIN 21 257
 FT PROPEP 258 281
 FT DOMAIN 44 207
 FT DOMAIN 111 118
 FT CARBOHYD 22 22
 FT CARBOHYD 36 36
 FT CARBOHYD 158 158
 FT CARBOHYD 230 230
 FT CARBOHYD 254 254
 FT CARBOHYD 255 255
 FT SEQUENCE 281 AA; 28992 MW; 50598AA42D64CCBC CRC64;
 Query Match 12.0%; Score 73; DB 1; Length 281;
 Best Local Similarity 35.8%; Pred. No. 4;
 Matches 24; Conservative 6; Mismatches 25; Indels 12; Gaps 3;
 QY 36 AATTWNSCICRDSGTDSDV-----DT-----QQQAENSVAPTADTRSPDRPVRPP 84
 DB 152 ANTEQNNSNVQDSQTSKSNVPTQADATKTSPTAQPEQAENSA-PTAEQTSPQLQSAPE 210
 QY 85 RRGGRPH 91
 DB 211 NKGTCQH 217
 RESULT 7
 TGN1_MOUSE
 ID TGN1_MOUSE STANDARD; PRT; 353 AA.
 AC Q62313.
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Trans-golgi network integral membrane protein 1 precursor (TGN38A).
 GN TGNL1 OR TGN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;

RX MEDLINE=95301533; PubMed=7540170;
 RA Kasai K., Takahashi S., Murakami K., Nakayama K.;
 RT "Strain-specific presence of two TGN38 isoforms and absence of TGN41
 RT in mouse.";
 RL J. Biol. Chem. 270:14471-14476 (1995).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta, and Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.W., Knapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.B., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gusincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butterfield A.S.N., Krzywinski M.F., Skalska U., Smailus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: May be involved in regulating membrane traffic to and
 CC from trans-Golgi network.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Primarily in trans-
 CC Golgi network. Cycles between the trans-Golgi network and the cell
 CC surface returning via endosomes (By similarity).
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- MISCELLANEOUS: Also found in strains BALB/c, C57BL/6 and DBA/2.
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 CC -----
 DR EMBL: D50031; BAA08757.1; -;
 DR EMBL: AK041302; BAC30896.1; -;
 DR EMBL: AK076586; BAC38404.1; -;
 DR EMBL: BC009143; AA09143.1; -;
 DR PIR: B56940; B56940.
 DR MGD; MGI:105080; Tgoln1.
 KW Signal; Transmembrane; Glycoprotein; Repeat; Golgi stack.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 353 TRANS-GOLGI NETWORK INTEGRAL MEMBRANE
 FT PROTEIN 1.
 FT DOMAIN 18 298 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 299 319 POTENTIAL.
 FT DOMAIN 320 353 CYTOPLASMIC (POTENTIAL).
 FT SITE 346 349 ENDOCYTOSIS SIGNAL (BY SIMILARITY).
 FT DOMAIN 131 178 6 X 8 AA TANDDEM REPEATS.
 FT REPEAT 131 138 1.
 FT REPEAT 139 146 2.
 FT REPEAT 147 154 3.
 FT REPEAT 155 162 4.
 FT REPEAT 163 170 5.
 FT REPEAT 171 178 6.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 353 AA; 37848 MW; 95C340C2F4A21EB3 CRC64;
 Query Match 12.0%; Score 73; DB 1; Length 353;
 Best Local Similarity 30.5%; Pred. NO. 5.1;
 Matches 18; Conservative 9; Mismatches 28; Indels 4; Gaps 1;
 QY 32 GTGGAATTGNSICRDSSTDSVDTQQQAENSAVPTADTRSQPRDVPVRRGRGP 90
 Db 148 GDSGKTEAGSNKATEDDSGKSTKVLDLRPTSKIS-----PDTESTKTKVQTEKGQKP 202
 RESULT 8
 CAL3 HUMAN STANDARD; PRT; 1466 AA.
 ID P02461; Q15112;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1 (III) chain precursor.
 GN COL3A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=89350838; PubMed=2764886;
 RA Ala-Kokko L., Kontusaari S., Baldwin C.T., Kuivaniemi H.,
 RA Prockop D.J.;
 RT "Structure of cDNA clones coding for the entire prepro alpha 1 (III)
 RT chain of human type III procollagen. Differences in protein structure
 RT from type I procollagen and conservation of codon preferences.";
 RL Biochem. J. 260:509-516 (1989).
 RN [2]
 RP SEQUENCE OF 149-1225 FROM N.A.
 RX MEDLINE=89386015; PubMed=2780304;
 RA Janeczko R.A., Ramirez F.;
 RT "Nucleotide and amino acid sequences of the entire human alpha 1
 RT (III) collagen.";
 RL Nucleic Acids Res. 17:6742-6742 (1989).
 RN [3]
 RP SEQUENCE OF 168-398.
 RX MEDLINE=77134724; PubMed=557335;
 RA Seyer J.M., Kang A.H.;
 RT "Covalent structure of collagen: amino acid sequence of cyanogen

RT bromide peptides from the amino-terminal segment of type III collagen
RL of human liver." ;
RN Biochemistry 16:1158-1164(1977).
RP [4]
RA REVISIONS.
RA Seyer J.M.;
RL Submitted (DEC-1977) to the PIR data bank.
RN [5]
RP SEQUENCE OF 399-727.
RX MEDLINE=7900343; PubMed=687591;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of five
RT consecutive CNBr peptides from type III collagen of human liver." ;
RL Biochemistry 17:3404-3411(1978).
RN [6]
RP SEQUENCE OF 728-964.
RX MEDLINE=8019828; PubMed=6245925;
RA Seyer J.M., Mainardi C., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of alpha 1
RT (III)-CB5 from type III collagen of human liver." ;
RL Biochemistry 19:1583-1589(1980).
RN [7]
RP SEQUENCE OF 950-1466 FROM N.A.
RX MEDLINE=88189827; PubMed=3357782;
RA Mankoo B.S., Daigleish R.;
RT "Human pro alpha 1(III) collagen: cDNA sequence for the 3' end." ;
RL Nucleic Acids Res. 16:2337-2337(1988).
RN [8]
RP REVISION TO 1184.
RX MEDLINE=89098346; PubMed=3211760;
RA Molyneux K., Daigleish R.;
RT "Human type III collagen 'variant' is a cDNA cloning artefact." ;
RL Nucleic Acids Res. 16:11833-11833(1988).
RN [9]
RP SEQUENCE OF 1065-1466 FROM N.A.
RX MEDLINE=85087944; PubMed=6096827;
RA Rosenbloom J., Brinker J.W., May M., Pihlajaniemi T., Morrow S.,
RL Loidl H.R., Myers J.C.;
RT "Molecular cloning and carboxyl-propeptide analysis of human type III
RT procollagen." ;
RL Nucleic Acids Res. 12:9383-9394(1984).
RN [10]
RP SEQUENCE OF 965-1200.
RX MEDLINE=81208139; PubMed=7016180;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of alpha
RT 1(III)-CB9 from type III collagen of human liver." ;
RL Biochemistry 20:2621-2627(1981).
RN [11]
RP SEQUENCE OF 1176-1466 FROM N.A.
RX MEDLINE=85157600; PubMed=2579949;
RA Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F.;
RT "Isolation of cDNA and genomic clones encoding human pro-alpha 1
RT (III) collagen. Partial characterization of the 3' end region of the
RT gene." ;
RL J. Biol. Chem. 260:4357-4363(1985).
RN [12]
RP SEQUENCE OF 1161-1200 FROM N.A.
RX MEDLINE=86187804; PubMed=3754462;
RA Miskulin M., Daigleish R., Kluge-Beckerman B., Rennard S.I.,
RA Tolstoehev P., Brantly M., Crystal R.G.;
RT "Human type III collagen gene expression is coordinately modulated
RT with the type I collagen genes during fibroblast growth." ;
RL Biochemistry 25:1408-1413(1986).
RN [13]
RP SEQUENCE OF 1-170 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=88303360; PubMed=3405773;
RA Tonan D., Rica G., de Crombrughe B.;
RT "Nucleotide sequence of a cDNA coding for the amino-terminal region
RT of human prepro alpha 1(III) collagen." ;
RL Nucleic Acids Res. 16:7201-7201(1988).
RN [14]
RP SEQUENCE OF 1-176 FROM N.A.
RX MEDLINE=89378752; PubMed=2777083;
RA Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;
RT "Cloning and analysis of the 5' portion of the human type-III
RT procollagen gene (COL3A1)." ;
RL Gene 78:255-265(1989).
RN [15]
RP REVIEW ON VARIANTS.
RX MEDLINE=97255959; PubMed=9101290;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
RT associated collagen (type IX), and network-forming collagen (type X)
RT cause a spectrum of diseases of bone, cartilage, and blood vessels." ;
RL Hum. Mutat. 9:300-315(1997).
RN [16]
RP VARIANT AORTIC ANEURYSM ARG-303, AND VARIANT THR-668.
RX MEDLINE=93293988; PubMed=8514866;
RA Tromp G., Wu Y., Prockop D.J., Madhathari S.L., Kleinert C.,
RA Faruqi J.J., Zhuang J., Noerregaard O., Darling R.C., Abbott W.M.,
RA Cole C.W., Jaakkola P., Rytynen M., Pearce W.H., Yao J.S.T.,
RA Majamaa K., Smullen S.N., Gatalica Z., Ferrell R.E., Jimenez S.A.,
RA Jackson C.B., Michels V.V., Kaye M., Kuivaniemi H.;
RT "Sequencing of cDNA from 50 unrelated patients reveals that mutations
RT in the triple-helical domain of type III procollagen are an
RT infrequent cause of aortic aneurysms." ;
RL J. Clin. Invest. 91:2539-2545(1993).
RN [17]
RP VARIANT THR-698.
RX MEDLINE=91045136; PubMed=2235526;
RA Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari S.,
RA Wu Y., Ganguly A., Prockop D.J.;
RT "G to A polymorphism in exon 31 of the COL3A1 gene." ;
RL Nucleic Acids Res. 18:6180-6180(1990).
RN [18]
RP VARIANT AORTIC ANEURYSM ARG-786.
RX MEDLINE=91056145; PubMed=2243125;
RA Kontusaari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.;
RT "A mutation in the gene for type III procollagen (COL3A1) in a family
RT with aortic aneurysms." ;
RL J. Clin. Invest. 86:1465-1473(1990).
RN [19]
RP VARIANT EDS-IV ARG-828.
RX MEDLINE=94016385; PubMed=8411057;
RA Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.;
RT "The substitution of glycine 661 by arginine in type III collagen
RT produces mutant molecules with different thermal stabilities and
RT causes Ehlers-Danlos syndrome type IV." ;
RL J. Med. Genet. 30:690-693(1993).
RN [20]
RP VARIANT EDS-IV SER-957.
RX MEDLINE=89109135; PubMed=2492273;
RA Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.;
RT "A single base mutation that substitutes serine for glycine 790 of
RT the alpha 1 (III) chain of type III procollagen exposes an arginine
RT and causes Ehlers-Danlos syndrome IV." ;
RL J. Biol. Chem. 264:1349-1352(1989).
RN [21]
RP VARIANT EDS-IV VAL-960.
RX MEDLINE=95268429; PubMed=7749417;
RA Tromp G., de Paeppe A., Nuytinck L., Madhathari S.L., Kuivaniemi H.;
RT "Substitution of valine for glycine 793 in type III procollagen in
RT Ehlers-Danlos syndrome type IV." ;
RL Hum. Mutat. 5:179-181(1995).
RN [22]
RP VARIANT EDS-IV GLU-1014.
RX MEDLINE=92316511; PubMed=1352273;
RA Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
RA Pope F.M.;
RT "A single base mutation in the gene for type III collagen (COL3A1)
RT converts glycine 847 to glutamic acid in a family with Ehlers-Danlos
RT syndrome type IV. An unaffected family member is mosaic for the
RT mutation." ;
RL Hum. Genet. 89:414-418(1992).

1	20	POTENTIAL.
21	238	MEROZOITE SURFACE ANTIGEN 2.
239	262	HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
44	188	POLYMORPHIC REGION.
91	98	POLY-THR.
22	22	N-LINKED (GLCNAC. . .) (POTENTIAL).
36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).
139	139	N-LINKED (GLCNAC. . .) (POTENTIAL).
211	211	N-LINKED (GLCNAC. . .) (POTENTIAL).
235	235	N-LINKED (GLCNAC. . .) (POTENTIAL).
236	236	N-LINKED (GLCNAC. . .) (POTENTIAL).
262 AA;	27374 MW;	72E0B2A315E9D154 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 262;
Best Local Similarity 37.5%; Pred. No. 4.1;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

39	TMGNSGICRDDSGTDDSV	-----DT-----QQQQAENSAVPTADTRSPQRDPVPPRRG 87
137	TQNNNV-QQDSQTKSNVPTQADTKSPTRQPEQAENSA-PTAEQTESPELQSAPEKNG 194	
88	RGPH 91	
195	TGQH 198	

RESULT 10
MSA2_PLAF7 STANDARD; PRT; 272 AA.
AAC P50498;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface antigen 2 precursor (MSA-2) (45 kDa merozoite surface antigen).
MSA2.
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
(1)
SEQUENCE FROM N.A.
MEDLINE=90205972; PubMed=2181307;
Smythe J.A., Peterson M.G., Coppel R.J., Saul A.J., Kemp D.J., Anders R.F.;
"Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodium falciparum";
Mol. Biochem. Parasitol. 39:227-234 (1990).
-!- FUNCTION: May play a role in the merozoite attachment to the erythrocyte.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Potential).
-!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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EMBL; M28891; AAA29686.1; .
DR InterPro; IPR001136; MSA_2.
DR Pfam; PF00985; MSA_2; 1.
DR Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat; GPI-anchor; Merozoite.
SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 248 MEROZOITE SURFACE ANTIGEN 2
FT PROPEP 249 272 HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).
DOMAIN 44 198 POLYMORPHIC REGION.
FT CHAIN 91 108 POLY-THR.
FT PROPEP 95 108

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Query Match          11.9%; Score 72.5; DB 1; Length 274;
Best Local Similarity 37.5%; Pred. No. 4.3;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY      39  TGNESCICRDSGTDSDV-----DT-----QQQAENSAVPTADTRSFQDFVRPFRRG 87
DB      149  TQNNNV-QQDSQTKSNVPTQDADTKSPAQEAENSA-PTAEQTESPELQSAPEKNG 206
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
          88  RQPH 91
          |||
          207  TQQH 210

RESULT 12
MSA2_PLAFG
ID      MSA2_PLAFG      STANDARD;      PRT;      287 AA.
AC      P19260;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
DE      Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 2)
DE      (Membrane protein PF7).
DE      MSA2.
GN      Plasmodium falciparum (isolate FCR-3 / Gambia).
OC      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5838;
[1]_RN      [1]_TaxID=5838;
SEQUENCE FROM N.A.
MEDLINE=90349616; PubMed=1696728;
RX      Elliott J.F., Albrecht G.R., Gilladoga A., Handunnetti S.M.,
RA      Neekayee J., Lallinger G., Minjas J.N., Howard R.J.;
RA      "Genes for Plasmodium falciparum surface antigens cloned by
RT      expression in COS cells.";
RT      Proc. Natl. Acad. Sci. U.S.A. 87:6363-6367(1990).
RN      [2]
SEQUENCE FROM N.A.
MEDLINE=91117264; PubMed=1990294;
RX      Fenton B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D.,
RA      Ridley R., Scaife J.G., McBride J.S.;
RA      "Structural and antigenic polymorphism of the 35- to 48-kilodalton
RT      merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
RT      falciparum.";
RT      Mol. Cell. Biol. 11:963-971(1991).
RN      [3]
SEQUENCE FROM N.A.
MEDLINE=91218903; PubMed=2030943;
RX      Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
RA      "Sequence comparison of allelic forms of the Plasmodium falciparum
RT      merozoite surface antigen MSA2.";
RT      Mol. Biochem. Parasitol. 43:211-220(1990).
CC      -!- FUNCTION: May play a role in the merozoite attachment to the
CC      erythrocyte.
CC      -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC      (potential).
CC      -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
-----
CC      EMBL; M28890; AAA29650.1; -
CC      EMBL; X53832; CAA37829.1; -
CC      EMBL; M60188; AAA29688.1; -
CC      PIR; B39615; B39615.
CC      InterPro; IPR001136; MSA_2.
CC      Pfam; PF00395; MSA_2; 1.
CC      Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
CC      GPI-anchor; Merozoite.
CC      SIGNAL      1      20      POTENTIAL.
CC      FT

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FT CHAIN 21 263 MEROZOITE SURFACE ANTIGEN 2.
FT PROPEP 264 287 HYDROPHOBIC, REMOVED DURING MATURATION
FT (BY SIMILARITY)
FT DOMAIN 44 213 POLYMORPHIC REGION.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 287 AA; 28555 MW; 3968B90DAA917AF8 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 287;
Best Local Similarity 37.5%; Pred. No. 4.5;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TWMNSICRDRDSDGSDSV-----DT-----QQQAENSAPTADTRSPQRPDVRPPRRG 87
DB 162 TQNSNV-QQDSQTKSNVPTQADTKSPTAQPEQAENSA-PTAQTESPELQSAPEKNG 219
QY 88 RGPB 91
DB 220 TQGH 223

RESULT 13
MSA2 PLAFI STANDARD; PRT; 300 AA.
AC Q03644;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2).
MSA2.
GN Plasmodium falciparum (isolate imr143).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=57268;
RN [1]
RX MEDLINE=91156685; PubMed=2000383;
RA Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
RA Kemp D.J., Anders R.F.;
RT "Structural diversity in the Plasmodium falciparum merozoite surface
antigen 2."
RL Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
CC -!- FUNCTION: May play a role in the merozoite attachment to the
erythrocyte.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC -----
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CC -----
CC EMBL; M59767; AAA29695.1; -.
CC InterPro; IPR001136; MSA_2.
CC Pfam; PF00985; MSA_2; 1.
CC Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
CC GPI-anchor; Merozoite.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 276 MEROZOITE SURFACE ANTIGEN 2.
CC PROPEP 277 300 HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).
CC POLYMORPHIC REGION.
CC DOMAIN 44 226 POLY-THR.
CC DOMAIN 129 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 28555 MW; 3968B90DAA917AF8 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 300;

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FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 30131 MW; A01E17D36075D7D6 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 300;
Best Local Similarity 37.5%; Pred. No. 4.8;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TWMNSICRDRDSDGSDSV-----DT-----QQQAENSAPTADTRSPQRPDVRPPRRG 87
DB 175 TQNSNV-QQDSQTKSNVPTQADTKSPTAQPEQAENSA-PTAQTESPELQSAPEKNG 232
QY 88 RGPB 91
DB 233 TQGH 236

RESULT 14
MSA2 PLAFZ STANDARD; PRT; 300 AA.
AC Q03645;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2).
MSA2.
GN Plasmodium falciparum (isolate mad71 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=70154;
RN [1]
RX MEDLINE=91156685; PubMed=2000383;
RA Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
RA Kemp D.J., Anders R.F.;
RT "Structural diversity in the Plasmodium falciparum merozoite surface
antigen 2."
RL Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
CC -!- FUNCTION: May play a role in the merozoite attachment to the
erythrocyte.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC -----
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CC -----
CC EMBL; M59768; AAA29696.1; -.
CC PIR; A39112; A39112.
CC InterPro; IPR001136; MSA_2.
CC Pfam; PF00985; MSA_2; 1.
CC Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
CC GPI-anchor; Merozoite.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 276 MEROZOITE SURFACE ANTIGEN 2.
CC PROPEP 277 300 HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).
CC POLYMORPHIC REGION.
CC DOMAIN 44 226 POLY-THR.
CC DOMAIN 129 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 300 AA; 30101 MW; E4116107747AA10D CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 300;

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Best Local Similarity 37.5%; Pred. No. 4.8; Mismatches 24; Conservative 6; Indels 21; Gaps 4;

QY 39 TMGNSICRDSGTDSDV-----DT-----QQQAENSAVPTADTRSQPRDFVRPPRRG 87
Db 175 TQNSNV-QQDSQTSKSNVPRQDADTKSPTAQPEQAENSA-PTAEQTSPQLQAPENKG 232

QY 88 RGP 91
Db 233 TGOH 236

RESULT 15

MSA2_PLAF9 STANDARD; PRT; 302 AA.
AC Q03994;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2).
GN MSA2.
OS Plasmodium falciparum (isolate tak 9).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=57276;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91117264; PubMed=1990294;
RA Fenton B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D.,
RA Ridley R., Scaife J.G., McBride J.S.;
RT "Structural and antigenic polymorphism of the 35- to 48-kilodalton
RT merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
RT falciparum";
RL Mol. Cell. Biol. 11:963-971(1991).
CC -!- FUNCTION: May play a role in the merozoite attachment to the
CC erythrocyte.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X53833; CAA37830.1; -
CC PIR; A39615; A39615.
CC InterPro; IPR001136; MSA_2.
CC Pfam; PF00985; MSA_2; 1.
CC Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
CC GPI-anchor; Merozoite.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 278 MEROZOITE SURFACE ANTIGEN 2.
FT PROPEP 279 302 HYDROPHOBIC, REMOVED DURING MATURATION
FT (BY SIMILARITY).
FT DOMAIN 44 228 POLYMORPHIC REGION.
FT DOMAIN 131 138 POLY-THR.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 302 AA; 30259 MW; 4E0A7EB08227CF66 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 302;

Best Local Similarity 37.5%; Pred. No. 4.8; Mismatches 24; Conservative 6; Indels 21; Gaps 4;

QY 39 TMGNSICRDSGTDSDV-----DT-----QQQAENSAVPTADTRSQPRDFVRPPRRG 87
Db 175 TQNSNV-QQDSQTSKSNVPRQDADTKSPTAQPEQAENSA-PTAEQTSPQLQAPENKG 232

Db 177 TQNSNV-QQDSQTSKSNVPRQDADTKSPTAQPEQAENSA-PTAEQTSPQLQAPENKG 234
QY 88 RGP 91
Db 235 TGOH 238

Search completed: April 2, 2004, 10:29:41
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:27:15 ; Search time 21 Seconds
(without alignments)
535.924 Million cell updates/sec

Title: US-10-002-796-9
Perfect score: 609
Sequence: 1 MIVFGWVFLASRLGQGL.....QNVGLVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	85.5	14.0	290	2 T22161	hypothetical prote
2	79	13.0	612	2 T37181	thiamin biosynthes
3	75.5	12.4	900	2 B87957	protein Y1066GD.7
4	75.5	12.4	948	2 T26417	hypothetical prote
5	75	12.3	278	2 S39110	merozoite surface
6	75	12.3	286	2 B45632	merozoite surface
7	73.5	12.1	91	2 FL0227	T-cell receptor bs
8	73	12.0	1466	1 CGH07L	collagen alpha 1(I
9	73	12.0	2218	2 B84683	hypothetical prote
10	72.5	11.9	265	2 T05085	hypothetical prote
11	72.5	11.9	272	2 G71618	merozoite surface
12	72.5	11.9	274	2 A45632	merozoite surface
13	72.5	11.9	287	2 B39615	merozoite 45K surf
14	72.5	11.9	300	2 A39112	merozoite 45K surf
15	72.5	11.9	302	2 A39615	merozoite 45K surf
16	72.5	11.9	347	2 B39112	merozoite 45K surf
17	72.5	11.9	458	2 S24457	hypothetical prote
18	72	11.8	707	2 T26218	hypothetical prote
19	72	11.8	1787	2 T20160	NS3a homolog - mur
20	71.5	11.7	390	2 A47312	hypothetical prote
21	71	11.7	210	2 T41982	transcription regu
22	71	11.7	1479	2 T17401	trithorax protein
23	70.5	11.6	3759	2 A35085	hypothetical prote
24	70	11.5	113	2 T24164	hypothetical prote
25	69.5	11.4	219	2 T19828	hypothetical prote
26	69.5	11.4	318	2 C84651	hypothetical prote
27	69.5	11.4	773	2 F90537	lipoprotein (impor
28	69	11.3	261	2 S26070	conserved hypothet
29	69	11.3	281	2 S26052	hypothetical prote

30	69	11.3	319	2 H98216	hypothetical prote
31	69	11.3	545	2 P84533	Mutator-like trans
32	69	11.3	775	2 B72074	hypothetical prote
33	69	11.3	775	2 C81594	hypothetical prote
34	69	11.3	775	2 D86549	hypothetical prote
35	69	11.3	876	2 P22219	polypeptide - hepa
36	68.5	11.2	361	2 B56940	integral membrane
37	68.5	11.2	788	2 T25061	hypothetical prote
38	68	11.2	85	2 JH0786	transcription fact
39	68	11.2	130	2 B45613	surface antigen FU
40	68	11.2	208	2 T46896	merozoite surface
41	68	11.2	272	2 T29446	hypothetical prote
42	68	11.2	351	2 T51513	hypothetical prote
43	68	11.2	445	2 A56043	steroid hormone re
44	68	11.2	482	2 A70963	hypothetical prote
45	68	11.2	504	2 S75134	cell division prot

ALIGNMENTS

RESULT 1

T22161
hypothetical protein F44D12.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22161
R:Colles, L.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19525
A:Accession: T22161
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-290 <WIL>
A:Cross-references: EMBL:Z68298; PIDN:CAA92602.1; GSPDB:GN00022; CESP:F44D12.6
A:Experimental source: clone F44D12
A:Genetics:
A:Gene: CESP:F44D12.6
A:Map position: 4
A:Introns: 19/3; 154/2; 198/3

Query Match		14.0%; Score 85.5; DB 2; Length 290;
Best Local Similarity		30.0%; Pred. No. 0.47;
Matches	27; Conservative	15; Mismatches 31; Indels 17; Gaps 5;
QY	24	EEHTAHLGTGGAAATWGN-SCICRDSGTD-----DSVDTQQQQAENSAPVPTADTRSQP 77
DB	154	DAHV-HWRETGLAFIIRSDACRSKDDGGCDTIDSQNSKEDQERSKYNSEMPJSD----- 207
QY	78	RDVPRPRRGPGHEPRRKQNVGDLVLT 107
DB	208	KPDRKQ-----ETPRRSKQRTFGPMPT 232

RESULT 2

T37181
thiamin biosynthesis protein thic SCQ11.11 [similarity] - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C:Accession: T37181
R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21598
A:Accession: T37181
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-612 <SEE>
A:Cross-references: EMBL:AL096823; PIDN:CAB46966.1; GSPDB:GN000070; SCQDB:SCQ11.11
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: thic; SCQDB:SCQ11.11
C:Superfamily: thiamin biosynthesis protein thic

Query Match 13.0%; Score 79; DB 2; Length 612;
 Best Local Similarity 31.2%; Pred. No. 4.6;
 Matches 30; Conservative 7; Mismatches 37; Indels 22; Gaps 4;

QY 39 TMGNSICRDSG--TDSVDVTOQQA-----ENSAVPTADTRSQPRDPVRP-----83
 DB 60 TNGQSVLYDTSGYTDLVDVTVRGLAPLRNWIARGDTBEYACRPVRPEDDGKHT 119

QY 84 -PRGRG-----PHEPRKKQNVGLVLDTLAVIR 112
 DB 120 SPRGGLRNLDVFPGRPRGRGDGNVQTLAYAR 155

RESULT 3
 B87957
 Protein Y106G6D.7 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: B87957
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: B87957
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-900 <STO>
 A:Cross-references: GB:chr_I; PIDN:CAA20980.1; PID:93880680; GSPDB:GN000019; CESP:Y106G6D
 C:Genetics:
 A:Gene: Y106G6D.7
 A:Map position: 1

Query Match 12.4%; Score 75.5; DB 2; Length 900;
 Best Local Similarity 31.7%; Pred. No. 16;
 Matches 20; Conservative 10; Mismatches 18; Indels 15; Gaps 2;

QY 50 SGTDSVDVTOQQAENSAVPTADTRSQPRDPVR-----PPRGRGPHPRKKQ 98
 DB 496 SHEDDDKSRSRWEN-----TSPISRPRSLRDNRDRSRSPFRRRRRSRSPRRREE 551

QY 99 NVD 101
 DB 552 HTD 554

RESULT 4
 T26417
 Hypothetical protein Y106G6D.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26417
 R:McMurray, A.
 submitted to the EMBL Data Library, September 1998
 A:Reference number: Z20211
 A:Accession: T26417
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-948 <SWIL>
 A:Cross-references: EMBL:AL031629; PIDN:CAA20980.2; GSPDB:GN000019; CESP:Y106G6D.7
 A:Experimental source: clone Y106G6D
 C:Genetics:
 A:Gene: CESP:Y106G6D.7
 A:Map position: 1
 A:Introns: 68/3; 160/3; 270/2; 624/2; 706/3; 888/3; 924/3

Query Match 12.4%; Score 75.5; DB 2; Length 948;
 Best Local Similarity 31.7%; Pred. No. 16;
 Matches 20; Conservative 10; Mismatches 18; Indels 15; Gaps 2;

QY 50 SGTDSVDVTOQQAENSAVPTADTRSQPRDPVR-----PPRGRGPHPRKKQ 98
 DB 496 SHEDDDKSRSRWEN-----TSPISRPRSLRDNRDRSRSPFRRRRRSRSPRRREE 551

DB 544 SHEDDDKSRSRWEN-----TSPISRPRSLRDNRDRSRSPFRRRRRSRSPRRREE 599

QY 99 NVD 101
 DB 600 HTD 602

RESULT 5
 S39310
 merozoite surface antigen - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
 C:Accession: S39310
 R:Ramamoji, R.; Ranasinghe, C.
 submitted to the EMBL Data Library, November 1993
 A:Description: Cycle ds DNA sequencing of a malaria parasite protein from infected blood
 A:Reference number: S39310
 A:Accession: S39310
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-278 <RAM>
 A:Cross-references: EMBL:X76087; NID:9434996; PID:g836639
 C:Superfamily: Epstein-Barr virus nuclear antigen
 C:Keywords: surface antigen

Query Match 12.3%; Score 75; DB 2; Length 278;
 Best Local Similarity 34.6%; Pred. No. 5;
 Matches 27; Conservative 6; Mismatches 25; Indels 20; Gaps 5;

QY 32 GTGGA-----ATTMGNSICRDSGTTDDSV-----DT-----QOQQAENSAVPTADT 73
 DB 139 GNGGVQKPNQANKETQNNNV-QQDSQTKSNVPTQDADTKSPTAQPEQANSA-PTAEQ 196

QY 74 RSQPRDPVRPRRGRGP 91
 DB 197 TSPFELQSAFENKGTGQH 214

RESULT 6
 B45632
 merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 C:Accession: B45632
 R:Marshall, V.M.; Coppel, R.L.; Anders, R.P.; Kemp, D.J.
 Mol. Biochem. Parasitol. 50, 181-184, 1992
 A:Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
 A:Reference number: A45632; MUID:92178286; PMID:1542312
 A:Accession: B45632
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-286 <MAR>
 A:Experimental source: isolate 311
 A:Note: sequence extracted from NCBI backbone (NCBI:85255, NCBI:85259)
 C:Superfamily: Epstein-Barr virus nuclear antigen
 C:Keywords: surface antigen

Query Match 12.3%; Score 75; DB 2; Length 286;
 Best Local Similarity 34.6%; Pred. No. 5.1;
 Matches 27; Conservative 6; Mismatches 25; Indels 20; Gaps 5;

QY 32 GTGGA-----ATTMGNSICRDSGTTDDSV-----DT-----QOQQAENSAVPTADT 73
 DB 147 GNGGVQKPNQANKETQNNNV-QQDSQTKSNVPTQDADTKSPTAQPEQANSA-PTAEQ 204

QY 74 RSQPRDPVRPRRGRGP 91
 DB 205 TSPFELQSAFENKGTGQH 222

RESULT 7
 PL0227
 T-cell receptor beta chain V region (V-beta-6.7a, PCR-1) - human (fragment)

C;Species: Homo sapiens (man)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 30-May-1997
 C;Accession: P0227
 R;Li, Y.; Szabo, P.; Robinson, M.A.; Dong, B.; Posnett, D.N.
 J. Exp. Med. 171, 221-230, 1990
 A;Title: Allelic variations in the human T cell receptor V-beta-6.7 gene products.
 A;Reference number: P0225; MUID:9011615; PMID:1967299
 A;Accession: P0227
 A;Molecule type: mRNA
 A;Residues: 1-91 <LIV>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: T-cell receptor

Query Match 12.1%; Score 73.5; DB 2; Length 91;
 Best Local Similarity 34.1%; Pred. No. 2.1;
 Matches 30; Conservative 8; Mismatches 21; Indels 29; Gaps 5;

QY 7 AVFLASSLGGGLLTLEHIAHFLGTGGATMGNSICRDPDSG-----TDDSV 56
 DB 10 ALVYRSLGGL-----EFLVY-----QGNS--APDASGLPSDFSRERTGGSV 53

QY 57 DT---QQQAENSAVPTADTRSPRPDV 81
 DB 54 STLTIQRTQEDSAVYLCAAMPVPRDPV 81

RESULT 8
 CGHUTL
 collagen alpha 1(III) chain precursor - human
 N;Alternate names: procollagen alpha 1(III) chain
 C;Species: Homo sapiens (man)
 C;Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
 C;Accession: S05272; S04642; P0011; S01726; S04887; A90399; A94562; I51868; S59511; A90399
 R;Prockop, D.J.
 submitted to the EMBL Data Library, February 1989
 A;Reference number: S05272
 A;Accession: S05272
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1240, 'V', 1242-1466 <PRC>
 A;Cross-references: EMBL:X14420; NID:G30057; PIDN:CAA32583.1; PID:G30058
 R;Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
 Biochem. J. 260, 509-516, 1989
 A;Title: Structure of cDNA clones coding for the entire prepro-alpha1(III) chain of human
 erences.
 A;Reference number: S04642; MUID:89350838; PMID:2764886
 A;Accession: S04642
 A;Molecule type: mRNA
 A;Residues: 1-1196 <ALA>
 A;Cross-references: EMBL:X14420; NID:G30057; PIDN:CAA32583.1; PID:G30058
 A;Note: the complete sequence is not shown
 R;Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
 Gene 78, 255-265, 1989
 A;Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene
 A;Reference number: P0011; MUID:89378752; PMID:2777083
 A;Accession: P0011
 A;Molecule type: DNA
 A;Residues: 1-176 <BEN>
 A;Cross-references: GB:M26939; NID:G180813; PIDN:AAA52040.1; PID:G180814
 R;Toman, P.D.; Ricca, G.A.; de Crombrughe, B.
 Nucleic Acids Res. 16, 7201, 1988
 A;Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pre
 A;Reference number: S01726; MUID:88303360; PMID:3405773
 A;Accession: S01726
 A;Molecule type: mRNA
 A;Residues: 1-170 <TOM>
 A;Cross-references: EMBL:X07240; NID:G30060; PIDN:CAA30229.1; PID:G30061
 A;Note: the authors translated the codon CAG for residue 154 as His
 R;Janeczko, R.A.; Ramirez, F.
 Nucleic Acids Res. 17, 6742, 1989
 A;Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
 A;Reference number: S04887; MUID:89386015; PMID:2780304
 A;Accession: S04887

A;Molecule type: mRNA
 A;Residues: 149-163, 'G', 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-634, '
 A;Cross-references: EMBL:X15332; NID:G29545; PIDN:CAA33387.1; PID:G930045
 A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide
 R;Seyer, J.M.; Kang, A.H.
 Biochemistry 16, 1158-1164, 1977
 A;Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptides
 A;Reference number: A90399; MUID:77134724; PMID:557335
 A;Accession: A90399
 A;Molecule type: protein
 A;Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294, 'S', 296-398 <SEY1>
 A;Experimental source: liver
 A;Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose
 R;Seyer, J.M.
 submitted to the Atlas, December 1977
 A;Reference number: A94562
 A;Accession: A94562
 A;Molecule type: protein
 A;Residues: 'V', 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398 <SEY2>
 A;Experimental source: liver
 A;Note: author submitted corrections to A90399
 R;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
 Am. J. Hum. Genet. 53, 62-70, 1993
 A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
 splicing.
 A;Reference number: I51868; MUID:93304430; PMID:8317500
 A;Accession: I51868
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 186-194 <ML>
 A;Cross-references: GB:S62925; NID:G386425; PIDN:AAD13937.1; PID:G4261637
 R;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
 Biochem. J. 311, 939-943, 1995
 A;Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3A
 A;Reference number: S59511; MUID:96067614; PMID:7487954
 A;Accession: S59511
 A;Molecule type: mRNA
 A;Residues: 302-423 <CHI>
 A;Cross-references: GB:S79877; NID:G1195576; PIDN:AAAB35615.1; PID:G1195577
 R;Seyer, J.M.; Kang, A.H.
 Biochemistry 17, 3404-3411, 1978
 A;Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe
 A;Reference number: A90414; MUID:79000343; PMID:687591
 A;Accession: A90414
 A;Molecule type: protein
 A;Residues: 399-675, 'N', 677-727 <SEY3>
 A;Experimental source: liver
 R;Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
 J. Biol. Chem. 266, 5256-5259, 1991
 A;Title: G to T transversion at position +5 of a splice donor site causes skipping of the
 A;Reference number: I55349; MUID:91161621; PMID:1672129
 A;Accession: I55349
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 537-605 <LEE>
 A;Cross-references: GB:M59312; NID:G180815; PIDN:AAA52041.1; PID:G180816
 R;Seyer, J.M.; Mainardi, C.; Kang, A.H.
 Biochemistry 19, 1583-1589, 1980
 A;Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from tyr
 A;Reference number: A90438; MUID:80198282; PMID:6246925
 A;Accession: A90438
 A;Molecule type: protein
 A;Residues: 728-895, 'A', 897-964 <SEY4>
 A;Experimental source: liver
 R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Chan,
 J. Biol. Chem. 265, 17070-17077, 1990
 A;Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping and
 A;Reference number: A38303; MUID:91009133; PMID:2145268
 A;Accession: A38303
 A;Molecule type: mRNA
 A;Residues: 861-1015 <COL>
 A;Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:G180878; PIDN:AAAB59383.1; PID:G3
 A;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syn

R;Mankoo, B.S.; Dalglish, R.
 Nucleic Acids Res. 16, 2337, 1988
 A>Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.
 A;Reference number: S02119; MUID:8818927; PMID:3357782
 A;Accession: S02119
 A>Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>
 A;Cross-references: EMBL:X06700; NID:G30053; PIDN:CAA29886.1; PID:G30054
 R;Seyer, J.M.; Kang, A.H.
 Biochemistry 20, 2621-2627, 1981
 A>Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from ty
 A;Reference number: A90446; MUID:81208139; PMID:7016180
 A;Accession: A90446
 A;Molecule type: protein
 A;Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157-
 A;Experimental source: liver
 R;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Mye
 Nucleic Acids Res. 12, 9393-9394, 1984
 A>Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollage
 A;Reference number: A93551; MUID:85087944; PMID:6096827
 A;Accession: A93551
 A;Molecule type: mRNA
 A;Residues: 1065-1155, 'P', 1157-1466 <LOI>
 A;Cross-references: EMBL:X01655; EMBL:X01742; NID:G29584; PIDN:CAA25821.1
 R;Miskulin, M.; Dalglish, R.; Kluge-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brand
 Biochemistry 25, 1408-1413, 1986
 A>Title: Human type III collagen gene expression is coordinately modulated with the type
 A;Reference number: I52393; MUID:86187804; PMID:3754462
 A;Accession: I52393
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1161-1200 <MIS>
 A;Cross-references: GB:M11146; NID:G180415; PIDN:AAA52003.1; PID:G180416
 R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
 A>Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
 A;Reference number: I59025; MUID:85216505; PMID:3858826
 A;Accession: I79359
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1165-1196 <EMA>
 A;Cross-references: GB:M11134; NID:G180417; PIDN:AAA52004.1; PID:G180418
 R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
 J. Biol. Chem. 260, 4357-4363, 1985
 A>Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(III) collagen.
 A;Reference number: A92516; MUID:85157600; PMID:2579949
 A;Accession: A92516
 A;Molecule type: DNA
 A;Residues: 1176-1240, 'V', 1242-1356, 'P', 1358-1466 <CHU>
 A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GB
 A;Experimental source: liver
 A;Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given
 A;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 A;Comment: About 15% of the lysines are 5-hydroxylated and some are subsequently
 C;Genetics:
 A;Gene: GDB:COL3A1
 A;Cross-references: GDB:118729; OMIM:120180
 A;Map position: 2q31-2q31
 A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
 A;Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan
 C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfide
 er of their length, is formed with desmosine cross-links made from lysine and allylsine
 C;Function:
 A;Description: structural component of extracellular fibrous polymer that maintains inte
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
 C;Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hyd
 P;1-23/Domain: signal sequence #status predicted <SIG>
 P;24-153/Domain: amino-terminal propeptide #status predicted <PRO>
 F;31-91/Domain: von Willebrand factor type C repeat homology <VWC>
 F;154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>
 F;154-167/Region: amino-terminal nonhelical telopeptide

F;168-1196/Region: helical
 F;1091-1093/Region: cell attachment (R-G-D) motif
 F;1197-1221/Region: carboxyl-terminal nonhelical telopeptide
 F;1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>
 F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
 P;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted
 F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F;161-1212/Modified site: allylsine (Lys) #status experimental
 F;263/Binding site: carboxylate (Lys) (covalent) #status experimental
 F;584-1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
 F;948-949/Cleavage site: Gly-Asp (collagenase) #status experimental
 F;1106/Binding site: carboxylate (Lys) (covalent) #status predicted
 Query Match 12.0%; Score 73; DB 1; Length 1466;
 Best Local Similarity 28.9%; Pred. No. 47;
 Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7;
 QY 16 GQGLLTLEH---IAHFLGTGGAATTMGNS-----CICRDSGT---DPS 55
 DB 8 GSWLLALLHPITLLAQAEVGGCSHLGQSVADRDVWKEPCQICVC--DSGSLCDDI 65
 QY 56 V-DTQQQAEAGVP-----TATRSQPRDPVPRGRGPHPR 94
 DB 66 ICDDQELDCPNRPIPFGECCAVCPQPTATPRPP-NGQFGQGP 108
 RESULT 9
 B84683
 hypothetical protein At2g29300 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: B84683
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: B84683
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-2218 <STO>
 A;Cross-references: GB:AE002093; NID:G4803953; PIDN:AAD29825.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g28300
 A;Map position: 2
 Query Match 12.0%; Score 73; DB 2; Length 2218;
 Best Local Similarity 29.9%; Pred. No. 73;
 Matches 29; Conservative 17; Mismatches 19; Indels 32; Gaps 7;
 QY 45 ICRDSS-----GDDSV--DTQQQAENSA---VPTADTRS---QPRDPVRPP--- 84
 DB 49 LCQTESPDSPQKGEGSERSLANDTSNPVENSSTLLPTSTQATVQPMPEVRPQSHT 108
 QY 85 -----RGRGPHPRKKQNVGLVLDLAVIRT 113
 DB 109 LKERTQIKRGRG--RPRKTDKALTPVSL--AVSRT 141
 RESULT 10
 T05085
 hypothetical protein T6K21.170 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
 C;Accession: T05085
 R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Bancroft, I.; Mewes, I.
 submitted to the Protein Sequence Database, February 1998
 A;Reference number: 215397
 A;Accession: T05085
 A;Molecule type: DNA

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A;Residues: 1-265 <BEV>
A;Cross-references: EMBL:AL021889
A;Experimental source: cultivar Columbia; BAC clone T6K21
C;Genetics:
A;Map position: 4
A;Introns: 37/3; 59/2; 93/3; 163/1; 192/1
A;Note: T6K21.170

Query Match      11.9%; Score 72.5; DB 2; Length 265;
Best Local Similarity 37.5%; Pred. No. 8.4;
Matches 36; Conservative 24; Mismatches 38; Indels 55; Gaps 9;

QY 2 IVFGWAVFLASR--SLQQGLLLLEBIAH-----FLG-----TGGAA 37
DB 112 VCIGYITLVAKOPSAG--GSLVTFQTKVHVEDYSKINTLVLYARLKSPPPDEEIGGAK 170

QY 38 TTWMSN-----CICKDDSGTDSVDTQQQAENSAPTADTRSPQRPV-----RPRRG 87
DB 171 TGLGSSILGTCIHPCSKSVSKSVETEEN-----VKQPNRLKARNAVFIRVRYYPNGK 224

QY 88 RGP-----HEPRKKQNVGLVLTFLAVIRTLVD 116
DB 225 RAPKNGHKKPR-----DRAIIKRTMD 247

RESULT 11
G71618
merozoite surface antigen MSP-2 PFB0300C - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 17-Nov-2000
C;Accession: G71618; A44950
R;Gardner, M.J.; Tetzelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
R;Ferreira, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: G71618
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-272 <GAR>
A;Cross-references: GB:AF001385; GB:AE001362; NID:g3845143; PID:AAC71849.1; PID:g384514
A;Experimental source: clone 3D7
R;Smythe, J.A.; Peterson, M.G.; Coppel, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F.
Mol. Biochem. Parasitol. 39, 227-234, 1990
A;Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodi
A;Reference number: A44950; MUID:90205972; PMID:2181307
A;Accession: A44950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54, 'T', 56-272 <SMY>
A;Cross-references: GB:M28891; NID:g160458; PID:g160459
C;Genetics:
A;Gene: PFB0300C
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

Query Match      11.9%; Score 72.5; DB 2; Length 272;
Best Local Similarity 37.5%; Pred. No. 8.6;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TWGNSCTCRDSDSGTDSV-----DT-----QQQAENSAPTADTRSPQRPDPVPRRG 87
DB 147 TQNNSNV-QQDSQTKSNVPTQDADTKPTAQPEQAENSA-PTAEQTSPESLOQAPENKNG 204

QY 88 RGP 91
DB 205 TGOH 208

RESULT 12
A45632
merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum

```

```

C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A45632
R;Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
Mol. Biochem. Parasitol. 50, 181-184, 1992
A;Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
A;Reference number: A45632; MUID:92178286; PMID:1542312
A;Contents: KF1916
A;Accession: A45632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <MAR>
A;Cross-references: GB:M73810; NID:g160484; PID:g160485
A;Note: sequence extracted from NCBI backbone (NCBI:85252, NCBIP:85257)
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

Query Match      11.9%; Score 72.5; DB 2; Length 274;
Best Local Similarity 37.5%; Pred. No. 8.7;
Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TWGNSCTCRDSDSGTDSV-----DT-----QQQAENSAPTADTRSPQRPDPVPRRG 87
DB 149 TQNNSNV-QQDSQTKSNVPTQDADTKPTAQPEQAENSA-PTAEQTSPESLOQAPENKNG 206

QY 88 RGP 91
DB 207 TGOH 210

RESULT 13
B39615
merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum)
N;Alternate names: membrane antigen pf7
C;Species: Plasmodium falciparum
C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 01-Dec-2000
C;Accession: B39615; A36018; B44950; A45613
R;Penton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Scaife
Mol. Cell. Biol. 11, 963-971, 1991
A;Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite sur
A;Reference number: A39615; MUID:91117264; PMID:1990294
A;Accession: B39615
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <FEN>
A;Cross-references: EMBL:X53833
A;Note: clone T9-94
R;Elliot, J.F.; Albrecht, G.R.; Galladoga, A.; Handunnetti, S.M.; Neequaye, J.; Lallings
Proc. Natl. Acad. Sci. U.S.A. 87, 6363-6367, 1990
A;Title: Genes for Plasmodium falciparum surface antigens cloned by expression in COS cel
A;Reference number: A36018; MUID:90349616; PMID:1696728
A;Accession: A36018
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <ELL>
A;Cross-references: GB:M28890; NID:g160406; PID:g160407
R;Smythe, J.A.; Peterson, M.G.; Coppel, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F.
Mol. Biochem. Parasitol. 39, 227-234, 1990
A;Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodi
A;Reference number: A44950; MUID:90205972; PMID:2181307
A;Accession: B44950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186, 'R', 188-287 <SMY>
A;Cross-references: GB:M28892; NID:g160488; PID:g160489
R;Fandeur, T.; Bonnefoy, S.; Mercereau-Puijalon, O.
Mol. Biochem. Parasitol. 47, 167-178, 1991
A;Title: In vivo and in vitro derived Palo Alto lines of Plasmodium falciparum are genet
A;Reference number: A45613; MUID:92049549; PMID:1944415
A;Accession: A45613
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 28, 'E', 30-186, 'R', 188-230, 'IH' <FAN>
A;Experimental source: Uganda Palo Alto strain, merozoite

```

A;Note: sequence extracted from NCBI backbone (NCBIP:65035)
 C;Superfamily: Epstein-Barr virus nuclear antigen
 C;Keywords: membrane protein; surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 287;
 Best Local Similarity 37.5%; Pred. No. 9.1; Indels 13; Gaps 4;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;
 QY 39 TMGNSCICRDSGTDDSV-----DT-----QQQAENSAVPTADTRSQPRDPVPPRRG 87
 Db 162 TQNSNV-QQDSQTKSNVPTQADTKSPTAQPEQAENSA-PTAEQTSPFQSAPEKNG 219
 QY 88 RGPH 91
 Db 220 TGOH 223

RESULT 14

A39112
 merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum) (isol
 C;Species: Plasmodium falciparum
 C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 17-Nov-2000
 C;Accession: A39112
 R;Synthe, J.A.; Coppal, R.L.; Day, K.P.; Martin, R.K.; Oduola, A.M.J.; Kemp, D.J.; Ander
 Proc. Natl. Acad. Sci. U.S.A. 88, 1751-1755, 1991
 A;Title: Structural diversity in the Plasmodium falciparum merozoite surface antigen 2.
 A;Reference number: A39112; MUID:91156685; PMID:2000383
 A;Accession: A39112
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-300 <SMY>
 A;Cross-references: GB:M59765
 C;Superfamily: Epstein-Barr virus nuclear antigen
 C;Keywords: surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 300;
 Best Local Similarity 37.5%; Pred. No. 9.5; Indels 13; Gaps 4;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSCICRDSGTDDSV-----DT-----QQQAENSAVPTADTRSQPRDPVPPRRG 87
 Db 175 TQNSNV-QQDSQTKSNVPTQADTKSPTAQPEQAENSA-PTAEQTSPFQSAPEKNG 232
 QY 88 RGPH 91
 Db 233 TGOH 236

RESULT 15

A39615
 merozoite 45K surface antigen precursor (clone T9-96) - malaria parasite (Plasmodium fal
 C;Species: Plasmodium falciparum
 C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 17-Nov-2000
 C;Accession: A39615; S13802
 R;Fenton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Scaif
 Mol. Cell. Biol. 11, 963-971, 1991
 A;Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite sur
 A;Reference number: A39615; MUID:91117264; PMID:1990294
 A;Accession: A39615
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-302 <FEN>
 A;Cross-references: EMBL:X53832
 C;Superfamily: Epstein-Barr virus nuclear antigen
 C;Keywords: surface antigen

Query Match 11.9%; Score 72.5; DB 2; Length 302;
 Best Local Similarity 37.5%; Pred. No. 9.6; Indels 13; Gaps 4;
 Matches 24; Conservative 6; Mismatches 21; Indels 13; Gaps 4;

QY 39 TMGNSCICRDSGTDDSV-----DT-----QQQAENSAVPTADTRSQPRDPVPPRRG 87
 Db 177 TQNSNV-QQDSQTKSNVPTQADTKSPTAQPEQAENSA-PTAEQTSPFQSAPEKNG 234

QY 88 RGPH 91
 Db 235 TGOH 238

Search completed: April 2, 2004, 10:31:06
 Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:25:15 ; Search time 54 Seconds
(without alignments)
612.186 Million cell updates/sec

Title: US-10-002-796-9
Perfect score: 609
Sequence: 1 MIVFGWAVFLASRLQGLL.....QNVDELVLTLAVIRLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	100.0	117	4	AAB31180 Amino aci
2	609	100.0	117	6	ABO25151 Novel hum
3	609	100.0	117	6	ABU67269 Novel hum
4	609	100.0	117	6	ABU72037 Novel hum
5	609	100.0	117	6	ABU67138 Novel hum
6	609	100.0	117	6	ABU79780 Human sec
7	609	100.0	117	6	ABO33583 Novel hum
8	609	100.0	117	6	ADA47181 Human sec
9	609	100.0	117	7	ABO44436 Human sec
10	609	100.0	117	7	ABO33460 Novel hum
11	609	100.0	117	7	ABO19838 Human sec
12	609	100.0	117	7	ADCI17875 Human PRO
13	609	100.0	117	7	ADCI10295 Human sec
14	609	100.0	117	7	ADCI1255 Human sec
15	609	100.0	117	7	ADD70521 Human sec
16	609	100.0	117	7	ADD39598 Human sec
17	609	100.0	117	7	ADD70044 Human sec
18	609	100.0	117	7	ADD37048 Human sec
19	609	100.0	117	7	ADD38165 Human sec
20	609	100.0	117	7	ADD39121 Human sec
21	609	100.0	117	7	ADD38644 Human sec
22	609	100.0	117	7	ADD40075 Human sec
23	609	100.0	117	7	ADCI0075 Human sec
24	609	100.0	117	7	ADCI19908 Human sec
25	609	100.0	117	7	ADCI49819 Human sec

26	609	100.0	117	7	ADCI1377 Human sec
27	609	100.0	117	8	ADCI1256 Human sec
28	609	100.0	117	8	ADCI1104 Human sec
29	609	100.0	118	3	AAI99341 Human PRO
30	609	100.0	118	4	AAI66090 Protein O
31	609	100.0	118	5	ABBA4819 Human PRO
32	609	100.0	118	5	ABBA4819 Human PRO
33	609	100.0	118	5	ABBA4819 Human PRO
34	609	100.0	118	5	ABBA4819 Human PRO
35	609	100.0	118	5	ABBA4819 Human PRO
36	609	100.0	118	5	ABBA4819 Human PRO
37	609	100.0	118	5	ABBA4819 Human PRO
38	609	100.0	118	5	ABBA4819 Human PRO
39	609	100.0	118	5	ABBA4819 Human PRO
40	609	100.0	118	5	ABBA4819 Human PRO
41	609	100.0	118	5	ABBA4819 Human PRO
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43	609	100.0	118	5	ABBA4819 Human PRO
44	609	100.0	118	5	ABBA4819 Human PRO
45	609	100.0	118	5	ABBA4819 Human PRO

ALIGNMENTS

RESULT 1
AAB31180
ID AAB31180 standard; protein; 117 AA.
XX
AC AAB31180;
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of human polypeptide PRO444.
XX
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO242; PRO288; PRO365; PRO361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO170; PRO248; PRO337; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
XX
OS Homo sapiens.

Key	Location/Qualifiers
Peptide	1..16
FT	/note= "signal peptide"
FT	Modified-site 18..24
FT	/note= "N-myristoylation site"
FT	Modified-site 32..38
FT	/note= "N-myristoylation site"
FT	Modified-site 34..40
FT	/note= "N-myristoylation site"
FT	Modified-site 35..41
FT	/note= "N-myristoylation site"
FT	Modified-site 51..57
FT	/note= "N-myristoylation site"
XX	WO200077037-A2.
XX	21-DEC-2000.
XX	22-MAY-2000; 2000WO-US014042.
XX	15-JUN-1999; 99US-0139695P.
XX	20-JUL-1999; 99US-0145070P.
XX	26-JUL-1999; 99US-0145698P.
XX	17-AUG-1999; 99US-0149396P.
XX	01-SEP-1999; 99WO-US020111.
XX	08-SEP-1999; 99WO-US020554.
XX	15-SEP-1999; 99WO-US021090.
XX	15-SEP-1999; 99WO-US021547.
XX	30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028365.
 PR 07-DEC-1999; 99US-01694959.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerecht ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX
 DR WPI; 2001-050091/06.
 DR N-PSDB; AAC86965.
 XX
 PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
 PT transmembrane polypeptide is useful for gene therapy and identification
 PT of related polypeptides.
 XX
 PS Claim 12, Fig 4; 244pp; English.
 XX
 CC The present sequence represents a human secreted and transmembrane
 CC polypeptide. The specification describes human polypeptides, designated
 CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
 CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO1710,
 CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO333, PRO301, PRO187,
 CC PRO337, PRO1411, PRO4356, PRO246, PRO285, PRO941, PRO10096, PRO6003,
 CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
 CC can be modulated with agents that bind to these polypeptides, resulting
 CC in the death of the cells. The polynucleotides encoding these
 CC polypeptides are useful in the recombinant production of the
 CC polypeptides, as a hybridisation probe to screen libraries to isolate
 CC homologous sequences, or to map the gene. They may also be used for
 CC analysing genetic disorders, and to produce transgenic animals which are
 CC useful for the development and screening of therapeutically useful
 CC reagents. The polynucleotides can also be used in gene therapy e.g. to
 CC replace a defective gene
 XX
 SQ Sequence 117 AA;
 Query Match 100.0%; Score 509; DB 4; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGWAVFLASRLGQGLLLTLESHIAFLGTGGAATTMGNSICRDSGTDSDVDTQQ 60
 Db 1 MIVFGWAVFLASRLGQGLLLTLESHIAFLGTGGAATTMGNSICRDSGTDSDVDTQQ 60
 QY 61 QAENSAPVPTATRSQPRDPVPPRRGRGPHEPRKKNQVGLVLDTLAVIRTLVXK 117
 Db 61 QAENSAPVPTATRSQPRDPVPPRRGRGPHEPRKKNQVGLVLDTLAVIRTLVXK 117
 RESULT 2
 ABO25151
 ID ABO25151 standard; protein; 117 AA.
 XX
 AC ABO25151;
 XX
 DT 05-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444.
 XX

KW Human; secreted and transmembrane protein; PRO; antidiabetic;
 KW ophthalmological; cytostatic; immunostimulant; gene therapy;
 KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
 KW protein secretion disorder; pancreas disorder; diabetes;
 KW vascular permeability; retinal neuron cell survival; retinal disorder;
 KW immune response; inflammation; mononuclear cell infiltration;
 KW eosinophil infiltration; apoptosis; neoplastic growth.
 XX
 OS Homo sapiens.
 XX
 XX US2003040014-A1.
 XX 27-FEB-2003.
 XX
 XX 01-FEB-2002; 2002US-00066269.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 03-FEB-1998; 98US-0074092P.
 PR 23-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0098601P.
 PR 10-SEP-1998; 98US-0098603P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US018824.
 PR 16-SEP-1998; 98WO-US019093.
 PR 17-SEP-1998; 98WO-US019310.
 PR 17-SEP-1998; 98US-0100588P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 25-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025190.
 PR 08-MAR-1999; 98WO-US025108.
 PR 23-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 26-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.

PR 20-MAR-2000; 2000WO-US0007377.
 PR 30-MAR-2000; 2000WO-US0008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US0008520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX

PA (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Klijavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX

DR WPI; 2003-503396/47.
 DR N-PSDB; ACD42316.

XX New secreted and transmembrane PRO polypeptides, useful for treating
 PT diabetes, retinal disorders and stimulating an immune response.

XX Claim 12; Fig 4; 25app; English.

XX The invention describes an isolated polypeptide (I) having at least 80 %
 CC amino acid sequence identity to 30 secreted and transmembrane
 CC polypeptides. PRO polypeptides are also useful for stimulating
 CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
 CC factor stimulated proliferation of endothelial cells, stimulating
 CC proliferation of stimulated T-lymphocytes and for inducing proliferation
 CC of PD12 pancreatic ductal cells and are thus useful in the treatment of
 CC disorders which involve protein secretion by the pancreas, including
 CC diabetes. PRO polypeptides are useful for inducing vascular permeability
 CC and in enhancing survival of retinal neurons cells and are thus useful
 CC for the treatment of retinal disorders. PRO polypeptides are also useful
 CC for stimulating an immune response and inducing inflammation by inducing
 CC mononuclear cell and eosinophil infiltration at the site of infection of
 CC an animal. The PRO polypeptides are further useful for inducing apoptosis
 CC in endothelial cells for inhibiting neoplastic growth. This is the amino
 CC acid sequence of a novel human secreted and transmembrane PRO polypeptide

XX Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLSGQLLLTLEHIAHFTGTGGAATTGNSICIRDDSGTDSVDTQ 60

Db 1 MIVFGWAVFLASRLSGQLLLTLEHIAHFTGTGGAATTGNSICIRDDSGTDSVDTQ 60

QY 61 QOANSAVPTADTRSQPRDPVPRRGGRGPHPRKQNVGLVLTAVIRTLVDK 117

Db 61 QOANSAVPTADTRSQPRDPVPRRGGRGPHPRKQNVGLVLTAVIRTLVDK 117

RESULT 3

ABU67269

ID ABU67269 standard; protein; 117 AA.

XX

AC ABU67269;

XX

DT 28-MAY-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO444.
 XX Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
 KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
 KW PRO4356; PRO2630; PRO285; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
 KW obesity; diabetes; insulinemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis.
 XX Homo sapiens.
 OS US2003032063-A1.
 PN 13-FEB-2003.
 PD 01-FEB-2002; 2002US-00066494.
 XX 26-AUG-1997; 97US-0056974P.
 XX 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062818P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0098013P.
 PR 10-SEP-1998; 98US-009803P.
 PR 10-SEP-1998; 98US-0098611P.
 PR 14-SEP-1998; 98US-0099812P.
 PR 16-SEP-1998; 98US-0099812P.
 PR 17-SEP-1998; 98US-0100859P.
 PR 17-SEP-1998; 98US-0100859P.
 PR 24-SEP-1998; 98US-0101943P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 25-NOV-1998; 98US-0109304P.
 PR 01-DEC-1998; 98US-0109304P.
 PR 08-MAR-1999; 98US-0109304P.
 PR 23-MAR-1999; 98US-0125778P.
 PR 02-JUN-1999; 98US-0125778P.
 PR 15-JUN-1999; 98US-0139695P.
 PR 20-JUL-1999; 98US-0145070P.
 PR 26-JUL-1999; 98US-0145698P.
 PR 17-AUG-1999; 98US-0149396P.
 PR 01-SEP-1999; 98US-02020111.
 PR 08-SEP-1999; 98US-02020594.
 PR 15-SEP-1999; 98US-02021090.
 PR 15-SEP-1999; 98US-02021547.
 PR 30-NOV-1999; 98US-02028313.
 PR 01-DEC-1999; 98US-02028301.
 PR 02-DEC-1999; 98US-02028565.
 PR 07-DEC-1999; 98US-0169495P.
 PR 20-DEC-1999; 98US-02030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005641.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX
 PA (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX
 DR WPI; 2003-341964/32.
 DR N-PSDB; ACA04925.
 XX
 PT Thirty seven nucleic acids encoding novel secreted and transmembrane PRO
 PT polypeptides, useful for modulating biological activity of cell
 PT expressing the polypeptide, and in chromosome and gene mapping.
 XX
 XX Claim 12; Fig 4; 255pp; English.
 XX
 CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO333, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
 CC PRO6003, PRO6004, PRO4356, PRO4630, PRO941, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (II) is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (I) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
 CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This is the amino acid
 CC sequence of a novel human secreted and transmembrane polypeptide
 CC associated oligonucleotide
 XX
 XX Sequence 117 AA;
 XX
 Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGWAVFLASRGQGLLLLEHIAFLGTGGAATMGNSICRDSDGSDSDVDTQQ 60
 Db 1 MIVFGWAVFLASRGQGLLLLEHIAFLGTGGAATMGNSICRDSDGSDSDVDTQQ 60

QY 61 QQAENSAVPTADTRSQPRDVRPPRRGRGPHPRRKQNVDTGLVLTAVIRTLVDK 117
 Db 61 QQAENSAVPTADTRSQPRDVRPPRRGRGPHPRRKQNVDTGLVLTAVIRTLVDK 117
 RESULT 4
 ABU72037
 ID ABU72037 standard; protein; 117 AA.
 AC ABU72037;
 XX
 DT 11-JUN-2003 (first entry)
 DE Novel human secreted and transmembrane protein PRO444.
 XX
 KW Human; secreted and transmembrane polypeptide; PRO;
 KW fibroblast growth factor receptor; PRO333; PRO301; PRO187; PRO337;
 KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
 KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
 KW toxin; radiolabel; antibody; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tissue typing.
 XX
 OS Homo sapiens.
 XX
 FN US2002177165-A1.
 XX
 ED 28-NOV-2002.
 XX
 PF 01-FEB-2002; 2002US-00065500.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063382P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069594P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0085398P.
 PR 18-AUG-1998; 98US-0087000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US013093.
 PR 16-SEP-1998; 98WO-US013330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.

PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US023278.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021056.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX
 PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Garney AL, Kijavini LJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX WPI; 2003-328482/31.
 DR N-PSDB; ACA60455.

XX Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, for identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.

Claim 12; Fig 4; 25app; English.

CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
 CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO411,
 CC PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor
 CC (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or
 CC PRO951 polypeptide, and for linking a bioactive molecule to a cell
 CC expressing the above polypeptides. The bioactive molecule, a toxin,
 CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
 CC identify other proteins or molecules involved in binding interaction. The
 CC polynucleotide (II) encoding (I) is useful in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, for generating
 CC transgenic animals or knockout animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, to
 CC construct hybridisation probes for mapping the gene which encodes the PRO
 CC and for the genetic analysis of individuals with genetic disorders, in
 CC gene therapy, for chromosome identification and as a chromosome marker.
 CC (I) and (II) are useful for tissue typing. This is the amino acid
 XX sequence of a novel human secreted and transmembrane PRO polypeptide
 XX Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFGWAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDSVDTQQ 60
 Db 1 MIVFGWAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDSVDTQQ 60
 QY 61 QOAEASVPTADTRSQPRDPVPRRGPGPHEPRKKQNVGLVLDTLAVIRTLVDK 117
 Db 61 QOAEASVPTADTRSQPRDPVPRRGPGPHEPRKKQNVGLVLDTLAVIRTLVDK 117

RESULT 5

ABU67138
 ID ABU67138 standard; protein; 117 AA.
 XX
 AC ABU67138;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
 KW PRO187; PRO337; PRO411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
 KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
 KW obesity; diabetes; insulinemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 FN US2003032062-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 01-FEB-2002; 2002US-00066273.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063323P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081043P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095988P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US018824.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.

25-NOV-1998; 98WO-US025190.
 01-DEC-1998; 98WO-US025108.
 08-MAR-1999; 98WO-US005028.
 23-MAR-1999; 99US-0125778P.
 02-JUN-1999; 99WO-US012252.
 15-JUN-1999; 99US-0139695P.
 20-JUL-1999; 99US-0145070P.
 26-JUL-1999; 99US-0145698P.
 17-AUG-1999; 99US-0149396P.
 01-SEP-1999; 99WO-US020111.
 08-SEP-1999; 99WO-US020594.
 15-SEP-1999; 99WO-US021090.
 30-NOV-1999; 99WO-US021547.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028562.
 07-DEC-1999; 99US-0169495P.
 20-DEC-1999; 99WO-US030999.
 05-JAN-2000; 2000WO-US000219.
 18-FEB-2000; 2000WO-US004341.
 18-FEB-2000; 2000WO-US004342.
 22-FEB-2000; 2000WO-US004414.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 09-MAR-2000; 2000WO-US006471.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 15-MAY-2000; 2000WO-US013358.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032678.
 28-FEB-2001; 2001WO-US006520.
 30-MAY-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 15-NOV-2001; 2001US-00002796.
 (GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 Wood WI, Zhang Z;
 WPI; 2003-341963/32.
 N-PSDB; ACA04445.
 New secreted and transmembrane polypeptide for modulating biological
 activity of a cell expressing the polypeptide, identifying agonists or
 antagonists of the polypeptide, and as molecular weight markers.
 Claim 12; Fig 4; 254pp; English.
 The invention describes an isolated, secreted and transmembrane
 polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 PRO333, PRO301, PRO187, PRO337, PRO1411, PRO1096, PRO246, PRO6307,
 PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
 factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 cell expressing the polypeptides. The bioactive molecule causes cell
 death. (ii) is useful as hybridisation probes, in chromosome and gene
 mapping, in generation of antisense RNA and DNA, in the preparation of
 PRO polypeptide, for generating transgenic animals or knockout animals
 which in turn are useful in the development and screening of
 therapeutically useful reagents, and for the genetic analysis of

CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (i) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (ii) is useful for treating obesity, diabetes
 CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This is the amino acid
 CC sequence of a novel human secreted and transmembrane polypeptide
 XX Sequence 117 AA;
 SQ
 Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. NO. 28-63; 0; Indels 0; Gaps 0;
 Matches 117; Conservative 0; Mismatches 0;
 Qy 1 MIVFGMAVFLASRLGQGLLLTLEHIAHFLGTGGAATTGNSICRDSGTDSDVDTQ 60
 Db 1 MIVFGMAVFLASRLGQGLLLTLEHIAHFLGTGGAATTGNSICRDSGTDSDVDTQ 60
 Qy 61 QQAENSAVPTADTRSPRGRGPHPRKQNVGLVLTAVIRTLVDR 117
 Db 61 QQAENSAVPTADTRSPRGRGPHPRKQNVGLVLTAVIRTLVDR 117
 RESULT 6
 ABU79780
 ID ABU79780 standard; protein; 117 AA.
 XX AC ABU79780;
 XX DT 19-JUN-2003 (first entry)
 XX DE Human secreted/transmembrane protein PRO444.
 XX KW Human; secreted protein; transmembrane protein; PRO; genetic disorder;
 XX gene therapy.
 XX OS Homo sapiens.
 XX PN US2003032057-A1.
 XX PD 13-FEB-2003.
 XX PF 15-NOV-2001; 2001US-00002796.
 XX PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0093988P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 03-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.

17-SEP-1998; 98US-0100858P.
 17-SEP-1998; 98WO-US019437.
 24-SEP-1998; 98US-0101922P.
 28-OCT-1998; 98US-0106032P.
 28-NOV-1998; 98US-0109304P.
 20-NOV-1998; 98WO-US024855.
 25-NOV-1998; 98WO-US025190.
 01-DEC-1998; 98WO-US025108.
 08-MAR-1999; 99WO-US005028.
 23-MAR-1999; 99US-0125778P.
 15-JUN-1999; 99US-0139695P.
 02-JUN-1999; 99US-0145070P.
 26-JUL-1999; 99US-0145698P.
 17-AUG-1999; 99US-0149396P.
 01-SEP-1999; 99WO-US020111.
 08-SEP-1999; 99WO-US020594.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 30-NOV-1999; 99WO-US028313.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028365.
 07-DEC-1999; 99US-0169495P.
 20-DEC-1999; 99WO-US030999.
 05-JAN-2000; 2000WO-US000219.
 18-FEB-2000; 2000WO-US004341.
 18-FEB-2000; 2000WO-US004342.
 22-FEB-2000; 2000WO-US004414.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 09-MAR-2000; 2000WO-US006471.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 15-MAY-2000; 2000WO-US013358.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 11-AUG-2000; 2000WO-US022031.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032878.
 28-FEB-2001; 2001WO-US006520.
 30-MAY-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 (GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
 Ferrata N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 Godowski PJ, Gurney AL, Klijavin IJ, Mather JP, Napier MA, Pan J,
 Paoni NF, Roy WA, Stewart TA, Tamas D, Watanabe CK, Williams PM,
 Wood WI, Zhang Z;
 WPI; 2003-341960/32.
 N-PSDB; ACA65586.

Novel secreted and transmembrane polypeptide for modulating biological
 activity of cell expressing the polypeptide, identifying agonists or
 antagonists of polypeptide, and as molecular weight markers.

Claim 12; Fig 4; 25pp; English.

The invention relates to an isolated, secreted/transmembrane polypeptide,
 termed PRO polypeptide, having at least 80% sequence identity to a
 sequence selected from any one of the 37 sequences appearing as ABU79779
 -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
 under any one of the ATCC numbers given in the specification. Also
 included are an isolated nucleic acid molecule having at least 80%
 sequence identity to a sequence selected from any one of the 37 cDNA

sequences defined in the specification (or encoding the mature PRO
 protein or a PRO protein extracellular domain), a PRO expression vector,
 a host cell comprising the vector, PRO fusion proteins, anti-PRO
 antibodies and a method for linking a bioactive molecule to a cell
 expressing the above PRO polypeptides, the bioactive molecule is a toxin,
 radiolabel or an antibody and causes the death of the cell. PRO or the
 antibody is useful for modulating at least one biological activity of
 cell expressing the above polypeptides. PRO is useful for identifying
 agonists or antagonists of PRO, for preparing a variant of PRO, as
 molecular weight markers for protein electrophoresis purpose and PRO
 nucleic acid is useful for recombinantly expressing those markers. PRO is
 also useful as therapeutic agent. PRO is useful in assays to identify
 other proteins or molecules involved in binding interaction. PRO nucleic
 acid is useful as hybridisation probes, in chromosome and gene mapping,
 in generation of antisense RNA and DNA, in the preparation of PRO
 polypeptide, in gene therapy, for generating transgenic animals or
 knockout animals which in turn are useful in the development and
 screening of therapeutically useful reagents, to construct hybridisation
 probes for mapping the gene which encodes the PRO and for the genetic
 analysis of individuals with genetic disorders, for chromosome
 identification, as a chromosome marker, and for generating probes for
 polymerase chain reaction (PCR), Northern analysis, Southern analysis and
 Western analysis. The antibody is useful in diagnostic assays for PRO,
 e.g. detecting its expression in specific cells, tissues or serum, for
 affinity purification of PRO from recombinant cell culture or natural
 sources. PRO or Ab is useful for the preparation of medicament for
 treating conditions which is responsive to the PRO polypeptide or anti-
 PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
 present sequence encodes a PRO polypeptide

Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFGWAVFLASRLSGQLLTLESHIAHFLGTGAATMGNSICRDSDGDDSDVDTQQ 60
 DB 1 MIVFGWAVFLASRLSGQLLTLESHIAHFLGTGAATMGNSICRDSDGDDSDVDTQQ 60
 QY 61 QQAENSAPVTADTRSQPRDPVPPRGRGPHPRKKNVDGLVLDLTAVRTLVDK 117
 DB 61 QQAENSAPVTADTRSQPRDPVPPRGRGPHPRKKNVDGLVLDLTAVRTLVDK 117

RESULT 7
 ABO33583
 ID ABO33583 standard; protein; 117 AA.
 XX ABO33583;
 AC ABO33583;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444.
 XX
 KW Human; secreted and transmembrane protein; PRO; angiogenesis;
 KW endothelial cell proliferation; wound healing; immune response;
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
 KW cardiac insufficiency disorder; calcium flux; inflammation;
 KW vascular endothelial growth factor-stimulated proliferation;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW nephropathy; Schanlein-Henoch purpura; celliac disease; Crohn's disease;
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
 KW pancreatic beta-cell precursor cell differentiation; thalassemias;
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
 KW cartilage disorder; sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2003073130-A1.
 XX
 XX 17-APR-2003.
 PD
 XX

PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US031522.
PR 24-AUG-2000; 2000WO-US031328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030875.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006665.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUL-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX XX
PA (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Fan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WI;
XX WPI; 2003-585293/55.
DR N-PSDB; ACD68242.
XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-
Query Match 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 2a-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MIVFGWAVFLASRLSGGLLLTLEEHIAFLGTGGAATTGNSCICRDSGTTDSVDVTDQ 60
Db 1 MIVFGWAVFLASRLSGGLLLTLEEHIAFLGTGGAATTGNSCICRDSGTTDSVDVTDQ 60
OY 61 QQAENSAVPTADTRSPRDPVPRPRGRGPHPRKKQNVGDLVLTAVIRTLVDK 117
Db 61 QQAENSAVPTADTRSPRDPVPRPRGRGPHPRKKQNVGDLVLTAVIRTLVDK 117
RESULT 8
ADA47181
ID ADA47181 standard; protein; 117 AA.
XX AC ADA47181;
XX 20-NOV-2003 (first entry)
XX Human secreted/transmembrane polypeptide PRO444.
XX human; secreted protein; transmembrane protein; PRO; VEGF inhibitor;
KW vascular endothelial growth factor; endothelial cell proliferation;
KW T-lymphocyte proliferation; endothelial cell apoptosis;
KW c-fos stimulation; pancreatic beta cell differentiation;
KW chondrocyte proliferation; glucose uptake; free fatty acid; FFA uptake;
KW tissue typing.
XX OS Homo sapiens.
XX US2003044844-A1.
XX 06-MAR-2003.
XX 01-FEB-2002; 2002US-00066211.
XX 26-AUG-1997; 97US-0056974P.
XX 17-SEP-1997; 97US-0059115P.
XX 18-SEP-1997; 97US-0059263P.
XX 19-SEP-1997; 97US-0059588P.
XX 17-OCT-1997; 97US-0062285P.
XX 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 97US-0074086P.
PR 09-FEB-1998; 97US-0074092P.
PR 25-MAR-1998; 97US-0079294P.
PR 08-APR-1998; 97US-0081049P.
PR 14-JUL-1998; 97US-00814552.
PR 10-AUG-1998; 97US-0095998P.
PR 18-AUG-1998; 97US-0097000P.
PR 09-SEP-1998; 97US-0099601P.
PR 10-SEP-1998; 97US-0099803P.
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PR 14-SEP-1998; 97US-0099812P.
PR 16-SEP-1998; 97US-0099812P.
PR 17-SEP-1998; 97US-0100858P.
PR 17-SEP-1998; 97US-0100858P.
PR 24-SEP-1998; 97US-0101922P.
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PR 25-NOV-1998; 97US-0109304P.
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PR 02-JUN-1999; 97US-0125778P.
PR 15-JUN-1999; 97US-0139695P.
PR 20-JUL-1999; 97US-0145070P.
PR 26-JUL-1999; 97US-0145698P.
PR 17-AUG-1999; 97US-0149396P.
PR 01-SEP-1999; 97US-0202011.
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PR 15-SEP-1999; 97US-02021090.
PR 15-SEP-1999; 97US-02021547.
PR 30-NOV-1999; 97US-0208313.
PR 01-DEC-1999; 97US-0208313.
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PR 07-DEC-1999; 97US-0169495P.
PR 20-DEC-1999; 97US-0303099P.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
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PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI

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PR 02-SEP-1998; 98US-0098843P.
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PR 12-APR-1999; 99US-00284291.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-014758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 18-OCT-1999; 99US-00403297.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.

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PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032578.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006866.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUN-2001; 2001WO-US021735.
XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Pi Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pi Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Pi Williams PM, Wood WI;
XX WPI; 2003-585292/55.
XX N-PSDB; ACD67888.
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
XX preparation of a medicament for treating a condition responsive to PRO
XX polypeptide, and as therapeutic agents e.g. vaccines.
XX Claim 12; Fig 4; 561pp; English.
XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (I), having at least 80% sequence identity to a sequence
Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MIVFGWAVFLASRLGQLLITLSEHIAHFLGTGGAATTMGNSICRDDSSTGSDVDTQ 60
Db 1 MIVFGWAVFLASRLGQLLITLSEHIAHFLGTGGAATTMGNSICRDDSSTGSDVDTQ 60
Qy 61 QQAENSAPVPTADTRSPQRPVPPRGPGPHPRKKQNVGDLVLTAVIRTLVDK 117
Db 61 QQAENSAPVPTADTRSPQRPVPPRGPGPHPRKKQNVGDLVLTAVIRTLVDK 117
RESULT 11
ABO19838
ID ABO19838 standard; protein; 117 AA.
XX AC ABO19838;
XX DT 29-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO444.
XX KW Human; PRO; secreted and transmembrane protein; gene therapy;
XX enterocolitis; gastrointestinal ulceration; skin disease; asthma;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
XX myotrophic lateral sclerosis; inflammatory disease; organ failure;
XX rheumatoid arthritis; multiple sclerosis; atherosclerosis; infertility;
XX cardiac injury; birth defect; premature aging; AIDS; cancer;
XX diabetic complication; wound repair.
XX OS Homo sapiens.
XX PN US2003044902-A1.
XX PD 06-MAR-2003.
XX PF 01-FEB-2002; 2002US-00066193.
XX PG 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063323P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
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PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 10-AUG-1998; 98US-0095988P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
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PR 14-SEP-1998; 98WO-US019093.
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PR 17-SEP-1998; 98US-0100588P.
PR 17-SEP-1998; 98WO-US019437.
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PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
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PR 23-AUG-2000; 2000WO-US023522.
PR 04-AUG-2000; 2000WO-US023328.
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PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
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WPI; 2003-492261/46.
N-PSDB: ACD30202.

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease.

Claim 21; Fig 4: 154pp; English.

The invention relates to an isolated native sequence PRO polypeptide (secreted and transmembrane protein) having 80% sequence similarity to one of 37 proteins sequences (or PRO lacking its signal peptide, a PRO extracellular domain (with or without a signal peptide) encoded by a nucleic acid 80% identical to one of 37 cDNA sequences, shown in the specification. Also included are vectors comprising the PRO nucleic acids, host cells comprising the vectors (used to produce the PRO proteins), a chimeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence, an anti-PRO antibody, linking a bioactive molecule to a cell expressing the PRO polypeptides and modulating at least one biological activity of a cell expressing the polypeptides. The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, Gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications, or mutations in general. The polypeptides are also useful for wound repair and associated therapies concerned with re-growth of tissue. The nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents a PRO protein of the invention.

Sequence 117 AA:

```
Query Match      100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MIVFGWAVFLASRSLGOGLLLTLEEHIAHFLGTGGAATTMGNSCICRDPDSDSDVDT00 60

1 MIVFGWAVFLASRSLGOGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSDVDTQQ 60

61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHPRKKQNDGLVLDTLAVIRTLVDK 117

61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPFEP RRKKQNV DGLVLDTLAVIRTLVDK 117

RESULT 12

ADC17875

ID ADC17875 standard; protein; 117 AA.

AC ADC17875;

XX

DT	18-DEC-2003	(first entry)
DE		
XX	Human PRO polypeptide #2.	
XX		
KW	Human; PRO; protein electrophoretic disorder.	
KW		
XX		
OS	Homo sapiens.	
XX		
PN	US2003064925-A1.	
XX		
PD	03-APR-2003.	
PF		
XX	10-DEC-2001; 2001US-00013907.	
XX		
PR	01-SEP-1998; 98US-0098716P.	
PR	01-SEP-1998; 98US-0098723P.	
PR	01-SEP-1998; 98US-0098749P.	
PR	01-SEP-1998; 98US-0098750P.	
PR	02-SEP-1998; 98US-0098803P.	
PR	02-SEP-1998; 98US-0098821P.	
PR	02-SEP-1998; 98US-0098843P.	
PR	09-SEP-1998; 98US-0098933P.	
PR	09-SEP-1998; 98US-0098956P.	
PR	09-SEP-1998; 98US-0098983P.	
PR	09-SEP-1998; 98US-0099020P.	
PR	09-SEP-1998; 98US-0099042P.	
PR	09-SEP-1998; 98US-0099741P.	
PR	10-SEP-1998; 98US-0099754P.	
PR	10-SEP-1998; 98US-0099763P.	
PR	10-SEP-1998; 98US-0099792P.	
PR	10-SEP-1998; 98US-0099808P.	
PR	10-SEP-1998; 98US-0099812P.	
PR	10-SEP-1998; 98US-0099815P.	
PR	10-SEP-1998; 98US-0099816P.	
PR	15-SEP-1998; 98US-0099835P.	
PR	15-SEP-1998; 98US-0100388P.	
PR	15-SEP-1998; 98US-0100390P.	
PR	16-SEP-1998; 98US-0100584P.	
PR	16-SEP-1998; 98US-0100627P.	
PR	16-SEP-1998; 98US-0100661P.	
PR	16-SEP-1998; 98US-0100662P.	
PR	16-SEP-1998; 98US-0100664P.	
PR	17-SEP-1998; 98US-0100683P.	
PR	17-SEP-1998; 98US-0100684P.	
PR	17-SEP-1998; 98US-0100710P.	
PR	17-SEP-1998; 98US-0100711P.	
PR	17-SEP-1998; 98US-0100919P.	
PR	17-SEP-1998; 98US-0100930P.	
PR	18-SEP-1998; 98US-0100848P.	
PR	18-SEP-1998; 98US-0100849P.	
PR	18-SEP-1998; 98US-0101014P.	
PR	18-SEP-1998; 98US-0101068P.	
PR	18-SEP-1998; 98US-0101071P.	
PR	22-SEP-1998; 98US-0101279P.	
PR	23-SEP-1998; 98US-0101471P.	
PR	23-SEP-1998; 98US-0101472P.	
PR	23-SEP-1998; 98US-0101473P.	
PR	24-SEP-1998; 98US-0101738P.	
PR	24-SEP-1998; 98US-0101739P.	
PR	24-SEP-1998; 98US-0101915P.	
PR	24-SEP-1998; 98US-0101916P.	
PR	24-SEP-1998; 98US-0102207P.	
PR	23-SEP-1998; 98US-0102240P.	
PR	23-SEP-1998; 98US-0102447P.	
PR	23-SEP-1998; 98US-0101447P.	
PR	23-SEP-1998; 98US-0101477P.	
PR	23-SEP-1998; 98US-0101479P.	
PR	24-SEP-1998; 98US-0101738P.	
PR	24-SEP-1998; 98US-0101741P.	
PR	24-SEP-1998; 98US-0101915P.	
PR	24-SEP-1998; 98US-0101916P.	
PR	23-SEP-1998; 98US-0102207P.	
PR	23-SEP-1998; 98US-0102240P.	
PR	23-SEP-1998; 98US-0102307P.	
PR	23-SEP-1998; 98US-0102330P.	
PR	30-SEP-1998; 98US-0102484P.	
PR	30-SEP-1998; 98US-0102484P.	

XX human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX Homo sapiens.
XX US2003105011-A1.
XX 05-JUN-2003.
XX 16-AUG-2002; 2002US-00223084.
XX 15-SEP-2000; 2000US-0232887P.
XX 20-JUN-2001; 2001WO-US019692.
XX 09-JUL-2001; 2001WO-US021735.
XX 20-FEB-2002; 2002US-00081056.
XX (GETH) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI: 2003-810831/76.
XX N-PSDB; ADD10294.
XX New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX Claim 11; SEQ ID NO 6; 493pp; English.
XX The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterized by the presence of
CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX Sequence 117 AA;
Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0;
QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDGSDSDVTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDGSDSDVTQQ 60
QY 61 QQAENSAPVTADTRSPQRPVPRPRGRGPHPRKKQNVGDLVLTAVIRLVDK 117
DB 61 QQAENSAPVTADTRSPQRPVPRPRGRGPHPRKKQNVGDLVLTAVIRLVDK 117
RESULT 14
ADD11255
ID ADD11255 standard; protein; 117 AA.
XX AC ADD11255;
XX

DT 01-JAN-2004 (first entry)
XX Human secreted/transmembrane PRO polypeptide #3.
DE human; secreted protein; transmembrane protein; cardiovascular disorder;
XX endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX Homo sapiens.
XX OS US2003105013-A1.
XX PN 05-JUN-2003.
XX PD 16-AUG-2002; 2002US-00223090.
XX PF 20-JUN-2001; 2001WO-US019692.
XX PR 09-JUL-2001; 2001WO-US021735.
XX PR 20-FEB-2002; 2002US-00081056.
XX (GETH) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI: 2003-801242/75.
XX N-PSDB; ADD11254.
XX New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, useful for treating a cardiovascular, endothelial, or
PT angiogenic disorder in a mammal, such as cancer or age-related macular
PT degeneration.
XX Claim 11; SEQ ID NO 6; 493pp; English.
XX The invention relates to an isolated nucleic acid encoding a secreted and
PS transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
XX by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterized by the presence of
CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX Sequence 117 AA;
Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0;
QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDGSDSDVTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSDGSDSDVTQQ 60
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DB 61 QQAENSAPVTADTRSPQRPVPRPRGRGPHPRKKQNVGDLVLTAVIRLVDK 117
RESULT 15
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ID ADD70521 standard; protein; 117 AA.

XX	ADD70521;	24-SEP-1998;	PR	98US-0101916P
XX	AC	29-SEP-1998;	PR	98US-0102207P
XX	XX	29-SEP-1998;	PR	98US-0102240P
XX	DT	29-SEP-1998;	PR	98US-0102307P
XX	DT	29-SEP-1998;	PR	98US-0102330P
DE	DE	29-SEP-1998;	PR	98US-0102331P
XX	XX	30-SEP-1998;	PR	98US-0102484P
KW	KW	30-SEP-1998;	PR	98US-0102487P
KW	KW	30-SEP-1998;	PR	98US-0102570P
KW	KW	30-SEP-1998;	PR	98US-0102571P
KW	KW	01-OCT-1998;	PR	98US-0102687P
KW	KW	01-OCT-1998;	PR	98US-0102687P
KW	KW	02-OCT-1998;	PR	98US-0102965P
KW	KW	06-OCT-1998;	PR	98US-0103258P
XX	XX	06-OCT-1998;	PR	98US-0103443P
OS	Homo sapiens.	07-OCT-1998;	PR	98US-0103314P
XX	XX	07-OCT-1998;	PR	98US-0103315P
PN	US2003099625-A1.	07-OCT-1998;	PR	98US-0103328P
PD	XX	07-OCT-1998;	PR	98US-0103395P
XX	29-MAY-2003.	07-OCT-1998;	PR	98US-0103396P
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XX	12-DEC-2001; 2001US-00015386.	07-OCT-1998;	PR	98US-0103401P
XX	XX	08-OCT-1998;	PR	98US-0103633P
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XX	98US-0098723P.	08-OCT-1998;	PR	98US-0103679P
PR	PR	08-OCT-1998;	PR	98US-0103711P
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PR	98US-0099602P.	27-OCT-1998;	PR	98US-0105881P
PR	09-SEP-1998;	27-OCT-1998;	PR	98US-0106023P
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PR	10-SEP-1998;	28-OCT-1998;	PR	98US-0106032P
PR	98US-0099763P.	28-OCT-1998;	PR	98US-0106033P
PR	10-SEP-1998;	28-OCT-1998;	PR	98US-0106178P
PR	98US-0099792P.	29-OCT-1998;	PR	98US-0106244P
PR	10-SEP-1998;	29-OCT-1998;	PR	98US-0106244P
PR	98US-0099808P.	29-OCT-1998;	PR	98US-0106384P
PR	10-SEP-1998;	29-OCT-1998;	PR	98US-0106384P
PR	98US-0099812P.	29-OCT-1998;	PR	98US-0106384P
PR	10-SEP-1998;	29-OCT-1998;	PR	98US-0106384P
PR	98US-0099815P.	30-OCT-1998;	PR	98US-0106464P
PR	10-SEP-1998;	30-OCT-1998;	PR	98US-0106464P
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PR	15-SEP-1998;	03-NOV-1998;	PR	98US-0106856P
PR	98US-0100385P.	03-NOV-1998;	PR	98US-0106902P
PR	15-SEP-1998;	03-NOV-1998;	PR	98US-0106902P
PR	98US-0100388P.	03-NOV-1998;	PR	98US-0106902P
PR	15-SEP-1998;	03-NOV-1998;	PR	98US-0106902P
PR	98US-0100390P.	03-NOV-1998;	PR	98US-0106902P


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PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WC-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WC-US020111.
PR 15-SEP-1999; 99WC-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WC-US028313.
PR 02-DEC-1999; 99WC-US028551.
PR 16-DEC-1999; 99WC-US030095.
PR 05-JAN-2000; 2000WC-US000219.
PR 06-JAN-2000; 2000WC-US000376.
PR 11-FEB-2000; 2000WC-US003565.
PR 18-FEB-2000; 2000WC-US004342.
PR 24-FEB-2000; 2000WC-US005004.
PR 02-MAR-2000; 2000WC-US005841.
PR 15-MAR-2000; 2000WC-US006884.
PR 17-MAY-2000; 2000WC-US013705.
PR 22-MAY-2000; 2000WC-US014042.
PR 30-MAY-2000; 2000WC-US014941.
PR 02-JUN-2000; 2000WC-US015264.
PR 23-AUG-2000; 2000WC-US023522.
PR 24-AUG-2000; 2000WC-US023328.
PR 08-NOV-2000; 2000WC-US030952.
PR 10-NOV-2000; 2000WC-US030873.
PR 01-DEC-2000; 2000WC-US032678.
PR 28-FEB-2001; 2001WC-US008520.
PR 01-MAR-2001; 2001WC-US008666.
PR 01-JUN-2001; 2001WC-US017800.
PR 20-JUN-2001; 2001WC-US019692.
PR 29-JUN-2001; 2001WC-US021066.
PR 03-JUL-2001; 2001WC-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WI,
XX
XX WPI; 2003-874602/81.
DR DR
DR N-PSDB; ADD70520.
XX
XX
XX Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
XX
XX Claim 12; SEQ ID NO 6; 553pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred No. 2e-63; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 0;
OY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDSGTDSDVDTQQ 60
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDSGTDSDVDTQQ 60
OY 61 QQAENSAVPTADTRSPRPGRGPHPRKKQNVGVLVDTLAVIRTLVDX 117
DB 61 QQAENSAVPTADTRSPRPGRGPHPRKKQNVGVLVDTLAVIRTLVDX 117

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Search completed: April 2, 2004, 10:29:12
Job time : 55 secs